

STIC-Biotech/ChemLib

173647

From: Shaw, Amanda Marie
Sent: Wednesday, December 07, 2005 11:54 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 10/713/137

Please search:

- 1) SEQ ID NO: 2 and 3 (each of these sequences is 24 nucleotides in length). Please limit the search results to nucleic acids that are of a length of 50 nucleotides or less.
- 2) SEQ ID NO: 1 (258 nucleotides in length)

The CRF has been entered:

http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10713137

Please provide a printout of the first 40 results.

Thank you,

Amanda Shaw
Patent Examiner
Art Unit 1634
Remsen 2E78
Mailbox: REM 2C70
571-272-8668

CRF

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
.STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 15:51:35 ; Search time 2143 Seconds
(without alignments)
6843.495 Million cell updates/sec

Title: US-10-713-137-1
Perfect score: 258
Sequence: 1 cagcgagtgatggcaagca.....ttgtcccgatggtgcatc 258

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.env.*
- 4: gb.cm.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	47758	8	DQ060518 Homo sapi
2	257.6	99.8	116026	14	AC131306 Homo sapi
3	257.6	99.8	136599	8	AC130289 Homo sapi
4	257.6	99.8	156907	8	AL354047 Homo sapi
5	246.6	95.6	259	6	CS101221 Sequence
6	236.8	91.8	602	8	X85766 H.sapiens N
7	176.4	68.4	257	8	AF375649 Ateles be
8	120.4	46.7	1152	6	BD097464 Method fo
9	120.4	46.7	3462	6	BD097463 Method fo
10	120.4	46.7	3595	8	HUMNOSIND
11	120.4	46.7	3855	8	HU05810 Homo sapien
12	120.4	46.7	3946	6	AX067221 Sequence
13	120.4	46.7	3946	8	HSU20141 Human induc
14	120.4	46.7	3963	8	HUMITONOS
15	120.4	46.7	4062	6	AR124185 Human mkNA
16	120.4	46.7	4062	6	CQ776352 Sequence
17	120.4	46.7	4062	6	CQ776469 Sequence
18	120.4	46.7	4062	6	AR270915 Sequence

19	120.4	46.7	4062	8	HSU31511 Human induc
20	120.4	46.7	4145	6	I15516 Sequence 1
21	120.4	46.7	4145	6	I61175 Sequence 1
22	120.4	46.7	4145	8	L09210 Homo sapien
23	120.4	46.7	4164	6	A39980 Sequence 1
24	120.4	46.7	4164	6	AR380862 Sequence
25	120.4	46.7	4164	8	HSINOSA
26	120.4	46.7	4467	6	CQ723665 Sequence
27	120.4	46.7	35764	11	AY046510 Adenovira
28	118.8	46.0	4150	6	AX067222 Sequence
29	118.8	46.0	4150	8	AF068236 Homo sapi
30	116	45.0	179504	14	AC158064 Homo sapi
31	102.8	39.8	2838	4	AF223942 Ovis arie
32	100.2	38.8	648	10	BV410321 S299P690F
33	99.6	38.6	647	4	SSU59390 Sus scrofa
34	98.8	38.3	38817	9	AF427516 Mus muscu
35	98.8	38.3	178443	9	AL592185 Mouse DNA
36	98.8	38.3	236456	14	AC036147 Mus muscu
37	98.4	38.1	163	9	RNO230468 Rattus no
38	98.4	38.1	110000	14	AC105495 Rattus no
39	98.4	38.1	240200	14	AC103040 Rattus no
40	98.4	38.1	314746	14	AC106421 Rattus no
41	98	38.0	3970	9	AF027180 Cavia por
42	94.8	36.7	413	9	AY297461 Mesocric
43	94.8	36.7	3441	9	RATNOSA
44	94.8	36.7	3442	9	AY211532 Rattus no
45	94.8	36.7	3444	9	RNU26686 Rattus norv

ALIGNMENTS

RESULT 1
DQ060518 Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes)
LOCUS DQ060518 47758 bp DNA linear PRI 23-MAY-2005
DEFINITION (NOS2A) gene, complete cds.

ACCESSION DQ060518.1 GI:66268800
VERSION DQ060518
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

REFERENCE 1 (bases 1 to 47758)
AUTHORS Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Baier,C.N.,
Rajkumar,N., Willa,H.T., Daniels,M., Downing,T.K., Stanaway,I.B.,
Nguyen,C.P., Gildersleeve,H., Cassidy,C.M., Johnson,E.J.,
Swanson,J.E., McFarland,I., Yool,B., Park,C. and Nickerson,D.A.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2005) Genome Sciences, University of Washington,

1705 NE Pacific, Seattle, WA 98195, USA

COMMENT To cite this work please use: NIEHS-SNPs, Environmental Genome

Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA

(URL: <http://egp.gs.washington.edu>).

FEATURES

source Location/Qualifiers

repeat_region 153..211

variation 343

repeat_region 510..585

variation 541

replace="a"


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Query Match      99.8%; Score 257.6; DB 8; Length 47758;
Best Local Similarity 99.6%; Pred. No. 2.3e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGACCACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 21382 CAGCGGAGTGATGGCAGACCACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 21441
QY 61 GGTACACAGATGCCAGATGCCAGCATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 120
DB 21442 GGTACACAGATGCCAGATGCCAGCATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 21501
QY 121 GTACCCGGCCAGCTCAGCCCGGCCCATTTGGGCGGGAGCCCGTGGTGAGCGAGTG 180
DB 21502 GTACCCGGCCAGCTCAGCCCGGCCCATTTGGGCGGGAGCCCGTGGTGAGCGAGTG 21561
QY 181 ACAGAGTGAGCCAGAGAGACAGCAGCCCGGGCTTACAGACTCACAGGGCCGCTCTT 240
DB 21562 ACAGAGTGAGCCAGAGAGACAGCAGCCCGGGCTTACAGACTCACAGGGCCGCTCTT 21621
QY 241 GTTCCCAGCTGTGCATC 258
DB 21622 GTTCCCAGCTGTGCATC 21639

RESULT 2
AC131306
LOCUS
DEFINITION
AC131306 Homo sapiens chromosome 17 clone RP11-1145F2 map 17, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
AC131306.1 GI:22325231
VERSION
AC131306 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 116026)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-1145F2
Unpublished
2 (bases 1 to 116026)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeIrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Minova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,

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Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27556
Center clone name: 1145_F2
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111511 bases at least Q40
Consensus quality: 113602 bases at least Q30
Consensus quality: 114471 bases at least Q20
Insert size: 182000; agarose-fp
Quality coverage: 15.7 in Q20 bases; agarose-fp
Quality coverage: 24.8 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1896: contig of 1896 bp in length
* 1897: gap of 100 bp
* 1997: contig of 989 bp in length
* 2986: gap of 100 bp
* 3086: contig of 1464 bp in length
* 4550: gap of 100 bp
* 4550: gap of 100 bp
* 5973: contig of 1324 bp in length
* 6074: gap of 100 bp
* 6074: contig of 1823 bp in length
* 7896: gap of 100 bp
* 7897: contig of 1791 bp in length
* 9787: gap of 100 bp
* 9788: contig of 2703 bp in length
* 12590: contig of 2076 bp in length
* 12591: gap of 100 bp
* 14666: contig of 100 bp
* 14767: gap of 100 bp
* 14867: contig of 12028 bp in length
* 26895: gap of 100 bp
* 26895: gap of 100 bp
* 44060: contig of 17066 bp in length
* 44061: gap of 100 bp
* 44161: contig of 71866 bp in length.
* 116026: contig of 71866 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="17"
/map="17"
/clone="RP11-1145F2"
/clone_lib="RP11-11 Human Male BAC"
1. 1896
/notes="assembly_fragment
clone_end:SP6
vector_side:left"
1897. 1896
misc_feature
gap

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/gap 2986..3085 /note="assembly_fragment"
/misc_feature 3086..4549 /estimated_length=100
/gap 4550..4649 /note="assembly_fragment"
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/gap 5974..6073 /note="assembly_fragment"
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/misc_feature 12691..14766 /estimated_length=100
/gap 14767..14866 /note="assembly_fragment"
/misc_feature 14867..26894 /estimated_length=100
/gap 26895..26994 /note="assembly_fragment"
/misc_feature 26995..44060 /estimated_length=100
/gap 44061..44160 /note="assembly_fragment"
/misc_feature 44161..116026 /estimated_length=100
ORIGIN
Query Match 99.8%; Score 257.6; DB 14; Length 116026;
Best Local Similarity 99.6%; Pred. No. 2e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCAAGCAGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 75442 CAGCGGAGTGATGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 75501
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCACGTGGATTCACTCAG 120
Db 75502 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCACGTGGATTCACTCAG 75561
Qy 121 GTACCCGGCCAGCCTCAGCCRCGGCCATTGGGGGGGAGCCCGTGGTGAGCCGAGTG 180
Db 75562 GTACCCGGCCAGCCTCAGCCACCGGCATTTGGGGGGGAGCCCGTGGTGAGCGAGTG 75621
Qy 181 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAAGGGCCCGCTTT 240
Db 75622 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAAGGGCCCGCTTT 75681
Qy 241 GTTCCCGAGCTGTGCATC 258
Db 75682 GTTCCCGAGCTGTGCATC 75699
RESULT 3
AC130289/c AC130289 136599 bp DNA linear PRI 23-JAN-2003
LOCUS AC130289
DEFINITION Homo sapiens chromosome 17, clone RP1-66C13, complete sequence.
ACCESSION AC130289
VERSION AC130289.11 GI:27877275
KEYWORDS HTG.

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SOURCE
ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 136599)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP1-66C13

Unpublished

2 (bases 1 to 136599)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 136599)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (09-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 136599)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 136599)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Doolley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramabamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

TITLE
 Direct Submission
 Submitted (23-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT
 On Jan 23, 2003 this sequence version replaced gi:27753735.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L27646
 Center clone name: 66_C_13

Only the first 136.6 kilobases of this clone are being submitted.
 The remainder overlaps accession number AC005697 (WICGR project L418).

FEATURES

source	Location/Qualifiers	
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	/db_xref="taxon:9606"	
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repeat_region	complement(1739..2597)	
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repeat_region	complement(2993..3226)	
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repeat_region	3227..7281	
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repeat_region	7484..7913	
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repeat_region	12249..12275	
repeat_region	/rpt_family="(TG)n"	
repeat_region	12617..12907	
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repeat_region	/rpt_family="AluSc"	
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repeat_region	14352..14637	
repeat_region	/rpt_family="AluSg"	
repeat_region	16018..16074	
repeat_region	/rpt_family="AT rich"	
repeat_region	complement(16218..16420)	
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repeat_region	16698..16723	

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repeat_region	17849..18163		
repeat_region	/rpt_family="AluSg"		
repeat_region	complement(18348..18637)		
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repeat_region	/rpt_family="LTR12B"	19228..20196	
repeat_region	/rpt_family="HERV9"	20197..24554	
repeat_region	/rpt_family="HERV9"	24545..24911	
repeat_region	/rpt_family="HERV9"	complement(24912..25156)	
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repeat_region	/rpt_family="HERV9"	complement(25467..25477)	
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repeat_region	27243..27546		
repeat_region	/rpt_family="LTR12B"	27548..27637	
repeat_region	/rpt_family="LTR30"	27638..27739	
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repeat_region	/rpt_family="L2"	complement(28165..28254)	
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repeat_region	/rpt_family="FLAM_A"	28998..29212	
repeat_region	/rpt_family="MIR"	29297..29586	
repeat_region	/rpt_family="AluSc"	complement(29717..30006)	
repeat_region	/rpt_family="AluSx"	complement(30190..30319)	
repeat_region	/rpt_family="L2"	complement(30796..32672)	
repeat_region	/rpt_family="L1ME1"		

Query Match	99.8%; Score 257.6; DB 8; Length 136599;
Best Local Similarity	99.6%; Pred. No. 1.9e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	

QY	1	CAGCGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT	60
DB	87934	CAGCGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT	87875
QY	61	GGCTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCATCAG	120
DB	87874	GGCTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCATCAG	87815
QY	121	GTACCGGGCCAGCCCTCAGCCCGGGGAGCCCGTGTGTGAGCCAGTG	180
DB	87814	GTACCGGGCCAGCCCTCAGCCCGGGGAGCCCGTGTGTGAGCCAGTG	87755
QY	181	ACAGAGTGGAGCCAGAGGAGACACAGCCCGGGCTTACAGACTCAGAGGGCCCGTCTT	240
DB	87754	ACAGAGTGGAGCCAGAGGAGACACAGCCCGGGCTTACAGACTCAGAGGGCCCGTCTT	87695
QY	241	GTTCCCGAGCTGTGCATC	258
DB	87694	GTTCCCGAGCTGTGCATC	87677

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RESULT 4
HS66C13/c
LOCUS
DEFINITION Homo sapiens chromosome 17 from PAC RPCI-1 66C13 map 17p11.2 region
ACCESSION D17S842-D17S953, complete sequence.
VERSION AL354047
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ramser, J., Mueller, I., Sudbrak, R., Kosiura, A., Langer, I.,
Steffens, C., Klein, M., Heilmann, K., Schuelzchen, S., Starke, A.,
Thompson, C., Radelof, U., Francis, F., Seraneki, P., Poustcka, A.,
Lehrach, H. and Reinhardt, R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 156907)
MOLGENR.
Direct Submission
Submitted (28-APR-2000) MOLGENR, Abt. Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
On Jun 19, 2001 this sequence version replaced gi:13752107.
Clone received from the Resource Centre of the Human Genome Project
at the Max-Planck-Institute for Molecular Genetics
contig 01 1..156907.
FEATURES
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/mol_type="genomic DNA"
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/chromosome="17"
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institute: Roswell Park Cancer Institute, creator: Pieter
de Jong, P. Ioannou"
/note="Region between markers D17S842-D17S953"
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misc_feature 156907
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ORIGIN
Query Match 99.8%; Score 257.6; DB 8; Length 156907;
Best Local Similarity 99.6%; Pred. No. 1.9e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Qy 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCCAACGTGGAATTCACCTCAG 120
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Qy 121 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGGCGGGAGCCCGTGTGAGCGAGTG 180
Db 87813 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGGCGGGAGCCCGTGTGAGCGAGTG 87754
Qy 181 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 240
Db 87753 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 87694
Qy 241 GTTCCCGCAGCTGTGCATC 258
Db 87693 GTTCCCGCAGCTGTGCATC 87676

RESULT 5
CS101221
LOCUS
DEFINITION Sequence 1 from Patent WO2005047540.
ACCESSION CS101221
VERSION CS101221.1 GI:67509718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Pasha, A.O. and Ahsan, A.
JOURNAL Method of detecting predisposition to high altitude pulmonary edema
Patent: WO 2005047540-A 1 26-MAY-2005;
COUNCIL Council of Scientific and Industrial Research (IN)
FEATURES
source
1..259
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.2%; Pred. No. 1.7e-46;
Matches 257; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Qy 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCCAACGTGGAATTCACCTCAG 120
Qy 121 GTACCCGGCCAGCTCAGCC-RCCGGCCATTGGGGCGGGAGCCCGTGTGAGCGAGT 179
Db 121 GTACCCGGCCAGCTCAGCC-RCCGGCCATTGGGGCGGGAGCCCGTGTGAGCGAGT 180
Qy 180 GACAGAGTGGAGCCCGCAGAGAGACGCGAGCCCGGGCTTACAGACTCAGAGGGCCCGCT 239
Db 181 GACAGAGTGGAGCCCGCAGAGAGACGCGAGCCCGGGCTTACAGACTCAGAGGGCCCGCT 240
Qy 240 TGTTCGCCAGCTGTGCATC 258
Db 241 TGTTCGCCAGCTGTGCATC 259

RESULT 6
HSNOS2E89
LOCUS
DEFINITION H. sapiens NOS2 gene, exon 8 and 9.
ACCESSION X85766
VERSION X85766.1 GI:1130725
KEYWORDS nitric oxide synthase; NOS2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Xu, W., Charles, I.G., Liu, L., Morcada, S. and Emson, P.
JOURNAL Molecular cloning and structural organization of the human
inducible nitric oxide synthase gene (NOS2)
PUBMED Biochem. Biophys. Res. Commun. 219 (3), 784-788 (1996)
REFERENCE 8645258
2 (bases 1 to 602)
AUTHORS Xu, W.
JOURNAL Direct Submission
TITLE Submitted (21-MAR-1995) W. Xu, Babraham Institute, MRC Group, Dept
of Neurobiology, Cambridge CB2 4AT, UK
COMMENT Sequence overlapping with that under the acc#X73029.

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JOURNAL	Submitted (02-MAY-2001) Departamento de Bioquimica, Universidade d
SAO PAULO, SP 05508-900, Brazil	
FEATURES	Location/Qualifiers
source	1. .257
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	/db_xref="taxon:118643"
	/chromosome="14"
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CDS	<1. .>66
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	/product="nitric oxide synthase 2A"
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	/db_xref="GI:16923453"
	/translation="YAGYQMPDGSIRGDPANVEFTQ"
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Query Match	68.4%; Score 176.4; DB 8; Length 257;
Best Local Similarity	91.2%; Pred. No. 2.4e-30;
Matches 186; Conservative	1; Mismatches 17; Indels 0; Gaps 0;
QY	55 TATGCTGGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCTTGGCCAACTGGAATTC 114
Db	1 TATGCTGGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCTTGGCCAACTGGAATTC 60
QY	115 ACTCAGGTACCCGGCCAGCTCAGCCRCGCGCATTTGGGGCGGGAGCCCCCGTGGTGAG 174
Db	61 ACTCAGGTACCCAAACCCAGCCTGGCGCCCGCCAGCCCTTGGGGCAGGGAGCCCCCGTGGTGAG 120
QY	175 CGAGTCAGAGATGGAGCCCGCAGAGAGACACGCGCCCGGCTTACAGACTCACAGGGGCC 234
Db	121 CGAGTCAGAGATGGAGCCCGCAGAGAGACACGCGTGGCCAGGCTTGCAGACTCATGGGGCC 180
QY	235 CGTCTTGTTCCTCCAGCTGTGCATC 258
Db	181 TGTCTGTTCCTCCAGCTGTGCATC 204
RESULT 8	
BD097464	1152 bp DNA linear PAT 27-AUG-2002
LOCUS	Method for screening of inhibitors of inducible nitrogen oxide
DEFINITION	synthetase activation.
ACCESSION	BD097464
VERSION	BD097464.1 GI:22643038
KEYWORDS	WO 0166791-A/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 1152)
AUTHORS	Ishii,Y., Ueda,Y., Iwami,M., Arakawa,H. and Not,Y.
TITLE	Method for screening of inhibitors of inducible nitrogen oxide
JOURNAL	synthetase activation
	Patent: WO 0166791-A 2 13-SEP-2001;
	FUJISAWA PHARMACEUTICAL CO LTD,YOSHINORI ISHII,YOSHIKO UEDA,MORITA
	IWAMI, HIROYUKI ARAKAWA,YOSHITADA NOTSU
COMMENT	OS Homo sapiens (human)
	PN WO 0166791-A/2
	PD 13-SEP-2001
	PF 09-MAR-2001 WO 2001JP001865
	PR 10-MAR-2000 JP 00P 72480
	PI YOSHINORI ISHII,YOSHIKO UEDA,MORITA IWAMI,HIROYUKI ARAKAWA, PT
	YOSHITADA NOTSU
	PC C12Q1/25,C12N15/52,G01N33/50,G01N33/15

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	/sex="male"
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	/cell_type="fibroblasts"
	/clone_lib="PLT6B cosmid library"
gene	137. .602
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exon	137. .278
	/genes="NOS2"
	/product="inducible nitric oxidase synthase"
exon	548. .602
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	/number=9
ORIGIN	
Query Match	91.8%; Score 236.8; DB 8; Length 602;
Best Local Similarity	94.6%; Pred. No. 2.7e-44;
Matches 244; Conservative	1; Mismatches 13; Indels 0; Gaps 0;
QY	1 CACGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
Db	159 CACGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 218
QY	61 GGCTACCGATGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 120
Db	219 GGCTACCGATGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 278
QY	121 GTACCGGGCCAGCTCAGCCGCCGCTTGGGGGGGAGCCCGTGTGAGCGAGTG 180
Db	279 GTACCGGGCCAGCTCAGCCGCCGCTTGGGGGGGAGCCCGTGTGAGCGAGTG 338
QY	181 ACAGATGGAGCCAGAGGAGACACGCGAGCCCGGCTTACAGACTCACAGGGCCGCTCT 240
Db	339 ACAGATGGAGCCAGAGGAGACACGCGAGCCCGGCTTACAGACTCACAGGGCCGCTCT 398
QY	241 GTTCCCCAGCTGTGCATC 258
Db	399 GTTCCCCAGCTGTGCATC 416
RESULT 7	
AF375649	257 bp DNA linear PRI 14-NOV-2001
LOCUS	Ateles belzebuth chamek nitric oxide synthase 2A (NOS2A) gene,
DEFINITION	partial cds.
ACCESSION	AF375649
VERSION	AF375649.1 GI:16923452
KEYWORDS	
SOURCE	Ateles belzebuth chamek (Chamek spider monkey)
ORGANISM	Ateles belzebuth chamek
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Euthera; Euarchontoglires; Primates; Platyrrhini;
	Cebidae; Ateleinae; Ateles.
REFERENCE	1 (bases 1 to 257)
AUTHORS	Suarez,H.N., Lima,C.R., Lemos,B., Bonvicino,C.R., Moreira,M.A. and
	Canavez,F.C.
TITLE	Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
	Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15,
	17 and 22
JOURNAL	Chromosome Res. 9 (8), 631-639 (2001)
PUBMED	1178686
REFERENCE	2 (bases 1 to 257)
AUTHORS	Canavez,F.C.
TITLE	Direct Submission


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QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 819 GGCTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 878
QY 121 GT 122
Db 879 CT 880

RESULT 15
LOCUS AR124185 4062 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6171856.
ACCESSION AR124185
VERSION AR124185.1 GI:14109546
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Thigpen,A., Hohmeier,H.-E., Newgard,C.B., Unger,R.H.,
Shimabukuro,M., Chen,G., Rhodes,C.J., Hugl,S.R. and Cousin,S.
TITLE Methods and compositions relating to no-mediated cytotoxicity
JOURNAL Patent: US 6171856-A 11 09-JAN-2001;
FEATURES
source
1..4062
/organism="unknown"
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ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCATCCGCTATGCT 60
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QY 61 GGCTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGCTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 16
LOCUS CQ776352 4062 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 38 from Patent EP1394274.
ACCESSION CQ776352
VERSION CQ776352.1 GI:45379742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 38 03-MAR-2004;
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCATCCGCTATGCT 909
QY 61 GGCTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGCTACCATGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 17
LOCUS CQ776469 4062 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 155 from Patent EP1394274.
ACCESSION CQ776469
VERSION CQ776469.1 GI:45379859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 155 03-MAR-2004;
FEATURES
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Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCATCCGCTATGCT 60
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QY 121 GT 122
Db 970 CT 971

RESULT 18
LOCUS AR270915 4062 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1478 from patent US 6500938.
ACCESSION AR270915
VERSION AR270915.1 GI:29702149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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Best Local Similarity 99.2%; Pred. No. 1.2e-17;
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DEFINITION Sequence 155 from Patent EP1394274.
ACCESSION CQ776469
VERSION CQ776469.1 GI:45379859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 155 03-MAR-2004;
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Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCATCCGCTATGCT 60
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QY 121 GT 122
Db 970 CT 971

RESULT 18
LOCUS AR270915 4062 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1478 from patent US 6500938.
ACCESSION AR270915
VERSION AR270915.1 GI:29702149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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WOX;

FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Qy 61 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 120
Db 910 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 969

Qy 121 GT 122
Db 970 CT 971

RESULT 19
LOCUS HSU31511 4062 bp mRNA linear PRI 11-MAR-1997
DEFINITION Human inducible nitric oxide synthase (NOS) mRNA, complete cds.
ACCESSION U31511
VERSION U31511.1 GI:951320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Park,C., Gnanotiti,C., Park,R. and Krishna,G.
TITLE Direct Submision
JOURNAL Submitted (11-JUL-1995) Chang-Shin Park, Lab. of Molecular Immunology, NHLBI, 9000 Rockville Pike, Bethesda, MD 20892-1760, USA

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
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gene
CDS

KKREIPLKVLVKAFLFACMLMRKTMASRVRVTLTFATETCKSEALAWDLGALPSCAFN PKVVCMDKVPRLSCLEBERLLVVTSTFGNGDCRNGEKLKLLFMLKELNNKRYAVP GLSSMYPRFCAFAHDIDOKLSHLGSQLTPMGEGDELSQEDAFRWSAVQTFRKAACE TFDVRGKHQIIPKLYTSNVTPHHYLVQDSQPLDLKSLSSMHAKNVFTMKLKR QNLQSTSSRATILVELSCEDGGLNYLPGHGLVCPGNQPALVQGLERLVVDGTPH QTVREALDESGSYWVSDKRLPPCSLSQALTYFLDITPTPTQLLLQLAQVATEPER ORLEALCOPSEYSKWKFTNSPTFLEVLBBPRLSVAGPLLSOLPIKPRFYSISSR DHPTRIHLTVAVVYTRDGOGLHHGVCSTWLSLKPODPVPCFVRNAGSPLHPD PSHPCILIGTGCTIAFRSFQWQRLHDSQHKVGRGRLVLFCCRDEDEHIIYQEEML EMAQGVLLHAVHTAYSLRPGKPKVYVODILRQQLASEVLRLVHKPEHGLXVCGDVRA RDVAHTLKQLVAAKLKLNBEQVEDYFFQLKSQKRYHEDIFGAVFPYBAKKDRVAQPS SLRMSAL"

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4047
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/note="16 A nucleotides"

ORIGIN
Query Match 46.7%; Score 120.4; DB 8; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

Qy 61 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 120
Db 910 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 969

Qy 121 GT 122
Db 970 CT 971

RESULT 20
LOCUS I15516 4145 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 1 from patent US 5468630.
ACCESSION I15516
VERSION I15516.1 GI:1250424
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4145)
AUTHORS Billiar,T.R., Nuseler,A.K., Geller,D.A. and Simmons,R.L.
TITLE cDNA clone for human inducible nitric oxide synthase and process for preparing same
JOURNAL Patent: US 5468630-A 1 21-NOV-1995;
FEATURES Location/Qualifiers
source 1..4145
/organism="unknown"
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ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010

Qy 61 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 120
Db 1011 GGCTACCAAGTCCAGATGCGCAGATCAGAGGAGCCCTGCCAACGTTGGAATTCACCTCAG 1070

Qy 121 GT 122
Db 1071 CT 1072

RESULT 21

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I61175
LOCUS       I61175                     4145 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION   Sequence 1 from patent US 5658565.
ACCESSION   I61175
VERSION     I61175.1      GI:2479123
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 4145)
AUTHORS     Billiar,T.R., Tzeng,E., Nussler,A.K., Geller,D.A. and Simmons,R.L.
TITLE       Inducible nitric oxide synthase gene for treatment of disease
JOURNAL     Patent: US 5658565-A 1 19-AUG-1997;
FEATURES     Location/Qualifiers
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               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      46.7%; Score 120.4; DB 6; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      |||
DB      951  CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
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QY      61  GGTACCATGCGAGATGGCAGCATCAGAGGGACCTGCCAAGTGAATTCATCTAG 120
      |||
DB      1011  GGTACCATGCGAGATGGCAGCATCAGAGGGACCTGCCAAGTGAATTCATCTAG 1070
      |||

QY      121  GT 122
DB      1071  CT 1072

RESULT 22
HUMINOSA
LOCUS       HUMINOSA                     4145 bp      mRNA      linear      PRI 06-JAN-1995
DEFINITION   Homo sapiens inducible nitric oxide synthase mRNA, complete cds.
ACCESSION   L09210
VERSION     L09210.1      GI:292241
KEYWORDS    inducible gene; nitric oxide synthase.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 4145)
AUTHORS     Geller,D.A., Lowenstein,C.J., Shapiro,R.A., Nussler,A.K., Di
            Silvio,M., Wang,S.C., Nakayama,D.K., Simmons,R.L., Snyder,S.H. and
            Billiar,T.R.
TITLE       Molecular cloning and expression of inducible nitric oxide synthase
            from human hepatocytes
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3491-3495 (1993)
PUBMED     7682706
COMMENT     Original source text: Homo sapiens cDNA to mRNA.
FEATURES     Location/Qualifiers
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               /cell_type="hepatocyte"
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               1..206
               /gene="inducible nitric oxide synthase"
               207..3668
               /gene="inducible nitric oxide synthase"
               /function="enzyme"
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               /protein_id="AA59171.1"

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CDS

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EHLARVEATKEIETTGTQUTGBELIPATQAWRNAPRCIGRTQMSNLOVPDASCS
TAREMFHICRHRYSTNNNGIRSAITVFPQSDGKHDFRVNNAQLIRIYAGVQMPDGS
IRGDPANVEFTQCLDGLGPKPKYGRFVPLVQLQANGRDPELFEIPDLVLDEVAEHL
KEYWFRLELKWYALPAVANMLLEVGLEFPFCGPNFYMGTEIGRVDFCDVQRYHL
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3669..4145
/gene="inducible nitric oxide synthase"

3' UTR
ORIGIN
Query Match      46.7%; Score 120.4; DB 8; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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DB      951  CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
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QY      61  GGTACCATGCGAGATGGCAGCATCAGAGGGACCTGCCAAGTGAATTCATCTAG 120
      |||
DB      1011  GGTACCATGCGAGATGGCAGCATCAGAGGGACCTGCCAAGTGAATTCATCTAG 1070
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QY      121  GT 122
DB      1071  CT 1072

RESULT 23
A39980
LOCUS       A39980                     4164 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION   Sequence 1 from Patent WO9423038.
ACCESSION   A39980
VERSION     A39980.1      GI:2296175
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 4164)
AUTHORS     Moncada,S.E., Charles,I.G. and Palmer,R.M.
TITLE       INDUCIBLE NITRIC OXIDE SYNTHASE AND GENE THEREFOR
JOURNAL     Patent: WO 9423038-A 1 13-OCT-1994;
PUBMED     WELLICOME FOUND (GB)
COMMENT     Other publication AU 6287894 941024.
FEATURES     Location/Qualifiers
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Qy 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 970 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
Qy 61 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 1030 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1089
Qy 121 GT 122
Db 1090 CT 1091

RESULT 26
LOCUS CQ723665 4467 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 9599 from Patent WO02068579.
ACCESSION CQ723665
VERSION CQ723665.1 GI:42284522
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 9599 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4467;
Best Local Similarity 99.2%; Pred. No. 1.1e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 745 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804
Qy 61 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 805 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 864
Qy 121 GT 122
Db 865 CT 866

RESULT 27
LOCUS AY046510 35764 bp DNA linear SYN 17-SEP-2001
DEFINITION Adenoviral expression vector Ad-hiNOS, complete sequence.
ACCESSION AY046510
VERSION AY046510.1 GI:15636799
KEYWORDS Adenoviral expression vector Ad-hiNOS
SOURCE Adenoviral expression vector Ad-hiNOS
ORGANISM other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 35764)
AUTHORS Shapiro,R., Gao,W., Treng,E., Robbins,P.D., Timoty,B.R. and
Gambotto,A.
TITLE Construction and characterization of a clinical grade adenoviral
vector encoding the human iNOS cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 35764)
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AUTHORS Shapiro,R., Gao,W., Treng,E., Robbins,P.D., Timoty,B.R. and
Gambotto,A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Surgery, University of Pittsburgh, 300
Technology Drive, Pittsburgh, PA 15219, USA
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adenoviral vector psi5"
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EVEGRRMGLETHKLASLADQAVREINAVIHSFOKONTIMDRSAAESPMKWQNE
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Best Local Similarity 99.2%; Pred. No. 8.4e-18;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 2008 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 2067
Qy 61 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 2068 GCGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 2127
Qy 121 GT 122
Db 2128 CT 2129
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RESULT 28
AX067222
LOCUS
DEFINITION
Sequence 3 from Patent WO0078946.
AX067222
ACCESSION
AX067222.1 GI:12544879
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1
AUTHORS
Keller,E.T., Gravenstein,S. and Hall,D.M.
TITLE
Treatment of viral influenza with antisense oligonucleotides
JOURNAL
Patent: WO 0078946-A 3 28-DEC-2000;
Eastern Virginia Medical School (US)
LOCATION/Qualifiers
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ORIGIN
Query Match 46.0%; Score 118.8; DB 6; Length 4150;
Best Local Similarity 98.4%; Pred. No. 2.7e-17;
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTCCGGGTGGGAATGCTCAGCTCCGCTATGCT 60
Db 979 CAGCGGAGTGATGCGAAGCAGCAGCTCCGGGTGGGAATGCTCAGCTCCGCTATGCT 1038
Qy 61 GGCTACCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 120
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Qy 121 GT 122
Db 1099 CT 1100
RESULT 29
AF068236
LOCUS
DEFINITION
Homo sapiens inducible nitric oxide synthase (NOS) mRNA, complete
cda.
AF068236
ACCESSION
AF068236.1 GI:3192916
VERSION
AF068236
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 4150)
AUTHORS
Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
Yoneyama,T., Hatakeyama,K., Geller,D.A., Mickle,D.A.G.,
Simmons,R.L. and Billiar,T.R.
TITLE
Dedifferentiated human ventricular cardiac myocytes express
inducible nitric oxide synthase mRNA but not protein in response to
IL-1, TNF, IFNgamma, and LPS
JOURNAL
J. Mol. Cell. Cardiol. 29 (4), 1153-1165 (1997)
PUBMED
9160867
REFERENCE
2 (bases 1 to 4150)
AUTHORS
Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,
Yoneyama,T., Hatakeyama,K., Geller,D.A., Mickle,D.A.G.,
Simmons,R.L. and Billiar,T.R.
TITLE
Direct Submision
JOURNAL
Submitted (26-MAY-1998) Pharmacology, Westf.Wilhelms-Univ.,
Domagstr. 12, Munster D-48149, Germany
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 2.7e-17;
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTCCGGGTGGGAATGCTCAGCTCATCGCTATGCT 60
Db 979 CAGCGGAGTGATGCCAAGCAGCAGCTCCGGGTGGGAATGCTCAGCTCATCGCTATGCT 1038
Qy 61 GGCTACCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 120
Db 1039 GGCTACCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 1098
Qy 121 GT 122
Db 1099 CT 1100
RESULT 30
AC158064/c
LOCUS
DEFINITION
Bos taurus clone CH240-54J11, WORKING DRAFT SEQUENCE, 16 unordered
pieces.
AC158064
AC158064.2 GI:68266847
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
Bos taurus (cow)
SOURCE
Bos taurus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 179504)
AUTHORS
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,M., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guernsey, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, S., Kovar, C., Kowitz, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Lousegged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muniadasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okwuonu, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinhilber, M., Strong, R., Sutton, A., Svatek, A., Tabors, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, J., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 179504)
Worley, K.C.

Direct Submission
Submitted (04-MAR-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 179504)
Cow Genome Sequencing Consortium.

Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 28, 2005 this sequence version replaced gi:60498836.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine

Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: EDEA
Center clone name: CH240-54J11
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 174250 bases at least Q40
Consensus quality: 175616 bases at least Q30
Consensus quality: 176727 bases at least Q20
Estimated insert size: 174799; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1552: contig of 1552 bp in length
* 1553 1602: gap of 50 bp
* 11784: contig of 10182 bp in length
* 11785 11834: gap of 50 bp
* 11835 58179: contig of 46345 bp in length
* 58180 58574: gap of 395 bp
* 58575 102955: contig of 44381 bp in length
* 102956 103005: gap of 50 bp
* 103006 111668: contig of 8663 bp in length
* 111669 111718: gap of 50 bp
* 111719 120507: contig of 8788 bp in length
* 120508 120557: gap of 50 bp
* 125884 125933: contig of 5327 bp in length
* 125934 129689: contig of 3756 bp in length
* 129690 129739: gap of 50 bp
* 129740 144940: contig of 15200 bp in length
* 144941 145284: gap of 345 bp
* 145285 171600: contig of 26316 bp in length
* 171601 171700: gap of unknown length
* 171701 172740: contig of 1040 bp in length
* 172741 172840: gap of unknown length
* 172841 173900: contig of 1060 bp in length
* 173901 174000: gap of unknown length
* 174001 175179: contig of 1179 bp in length
* 175180 175279: gap of unknown length
* 175280 176330: contig of 1051 bp in length
* 176331 176430: gap of unknown length
* 176431 178072: contig of 1642 bp in length
* 178073 178172: gap of unknown length
* 178173 179504: contig of 1332 bp in length.
* 179505
Location/Qualifiers
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58180. .58574
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FEATURES
Source

gap
gap
gap
gap
gap
gap
gap

The WGS reads were placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were annotated with alleles from the boxer and the breed or canid from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:
A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poodle sequence was placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.

Internal-WGA-discovery (i-WGA):
A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were defined as mismatch positions that had a base quality of >= 30 on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.

FEATURES

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/strain="GermanShepherd"
/db_xref="taxon:9615"
/map="4 9 22-578 34794085-34794641"
/clone_lib="GermanShepherd"
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STS

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Best Local Similarity 79.6%; Pred. No. 6.8e-13;
Matches 117; Conservative 1; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 410 CAACGAACTGATGGGAAGCATGACTTCCGAGTCTGGAAACCCAGCTCATCCGCTATGCT 351
Qy 61 GGCTACCAAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 120
Db 350 GGCTACCAAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 120
Qy 121 GTACCCGGCCAGCCTCAGCCRCGGC 147
Db 290 GTGCGAGATCCAGCCTTGGTGGTGAC 264

RESULT 33
SSU59390
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

SSU59390 647 bp mRNA linear MAM 14-JAN-1997
U59390
U59390
U59390.1 GI:1777979
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE

AUTHORS
TITLE
JOURNAL
Murtough, M.P., Pampusch, M.S., Harsch, S. and Bennaars, A.M.
Direct Submission
Submitted (27-MAY-1996) Vet. Pathobiol., Univ. of Minn., 1971
Commonwealth Ave., St. Paul, MN 55108, USA

FEATURES

source
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/db_xref="taxon:9823"
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ORIGIN

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Best Local Similarity 88.5%; Pred. No. 9.4e-13;
Matches 108; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Qy 61 GGCTACCAAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 120
Db 169 GGCTACCAAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 120
Qy 121 GT 122
Db 229 CT 230

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AF427516
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 38817)
Cofe, F., Levacher, B., Rique, H., Leopold, O., Boutin, J.A. and
Galizzi, J.-P.
Genomic structure of the murine inducible nitric oxide synthase
(i-NOS) gene
Unpublished
2 (bases 1 to 38817)
Cofe, F., Levacher, B., Rique, H., Leopold, O., Boutin, J.A. and
Galizzi, J.-P.
Direct Submission
Submitted (03-OCT-2001) Cellular and Molecular Pharmacology,
Servier Research Institute, 125, Chemin de Ronde, Croissy sur Seine
78290, France

REFERENCE

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Cofe, F., Levacher, B., Rique, H., Leopold, O., Boutin, J.A. and
Galizzi, J.-P.
Genomic structure of the murine inducible nitric oxide synthase
(i-NOS) gene
Unpublished
2 (bases 1 to 38817)
Cofe, F., Levacher, B., Rique, H., Leopold, O., Boutin, J.A. and
Galizzi, J.-P.
Direct Submission
Submitted (03-OCT-2001) Cellular and Molecular Pharmacology,
Servier Research Institute, 125, Chemin de Ronde, Croissy sur Seine
78290, France

FEATURES

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/strain="CD-1"
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mRNA


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Em:BG974882.1 Em:BY174336.1 Em:BY175860.1 Em:BY176421.1
Em:BY202059.1 Em:BY724147.1 Em:BY747653.1 Em:CD555051.1
match: cDNAs: Em:AF065921.2 Em:AF065922.2 Em:AF065923.2
Em:AY090567.1 Em:BC062378.1 Em:D12520.1 Em:M84373.1
Em:M92649.1 Em:U43428.1"
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VLDESGSYWKDKRLPPCSLSOALTVELDITPTTQLOLHLKARFATDTRORLEAL
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complement(176084. .176134),complement(175517. .175558),
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/gene="Nos2"
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complement(174332. .174494),complement(172035. .172181))
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Db 146223 CAGCGAGTGACGGCAACATGACTTCAGGCTCTGGAAATTCACAGCTCATCGGTACGCT 146282
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QY 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGACCTGCCAAGTGGAAATTCATCTCAG 120
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Db 146283 GGCTACAGATGCCAGATGGCAGCATCAGAGGATGCTGCCCTTGAGATTACCCAG 146342
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QY 121 GTACCGCGCCAGCTCAGCCRCGCCGCTATGGGGGGGGAGCC 164
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Db 146343 GTA-CTGACTCAGCTCTCTAGATCCCTGTGGCGAGGGAGCCC 146385
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RESULT 36
AC036147 236456 bp DNA linear HTG 27-FEB-2003
LOCUS Mus musculus chromosome 11 clone RP23-240G13 map 11, WORKING DRAFT
DEFINITION AC036147
SEQUENCE, 10 unordered pieces.
ACCESSION AC036147
VERSION AC036147.4 GI:28570424
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 236456)
AUTHORS Birren,B., Nusbaum,C. and Lander,B.
```

TITLE
JOURNAL
REFERENCE
AUTHORS

Mus musculus chromosome 11, clone RP23-240G13
Unpublished
2 (bases 1 to 236456)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPeeters,R.,
Meldrum,J., Meneus,L., Mhova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talanas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 236456)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
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Collamore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,
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Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Mhova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
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Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talanas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

Center project name: L8876
Center clone name: 240_G_13
----- Summary Statistics
Sequencing vector: M13; M77815; 40% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 23217 bases at least Q40
Consensus quality: 234384 bases at least Q30
Consensus quality: 235022 bases at least Q20
Insert size: 230000; agarose-fp
Insert size: 235556; sum-of-contigs

Quality coverage: 12.2 in Q20 bases; agarose-fp
Quality coverage: 12.0 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1
* 33985: contig of 33985 bp in length
* 33986
* 34085: gap of 100 bp
* 35130: contig of 1045 bp in length
* 34086
* 35230: gap of 100 bp
* 35131
* 38166: contig of 2936 bp in length
* 35231
* 38167
* 38266: gap of 100 bp
* 38267
* 41660: contig of 3394 bp in length
* 41661
* 41760: gap of 100 bp
* 41761
* 55510: contig of 13750 bp in length
* 55511
* 55610: gap of 100 bp
* 55511
* 68417: contig of 12807 bp in length
* 68418
* 141054: contig of 72537 bp in length
* 141055
* 141155: gap of 100 bp
* 141155
* 167738: contig of 26584 bp in length
* 167739
* 167838: gap of 100 bp
* 167839
* 203042: contig of 35204 bp in length
* 203043
* 203142: gap of 100 bp
* 203143
* 236456: contig of 33314 bp in length.

FEATURES
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/clone_lib="RPCI-23 Female Mouse BAC"
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clone end:SP6
vector side:left"
33986..34085
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misc_feature
34086..35130
/notes="assembly_fragment"
35131..35230
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/note="assembly_fragment"
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Matches 129; Conservative 1; Mismatches 33; Indels 1; Gaps 1;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGATGCTCAGCTCATCGGTATGCT 60
    |||||
Db 131611 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGATGCTCAGCTCATCGGTATGCT 60
    |||||

QY 61 GGCTACCAAGATGCCAGATGGCAGATCAGAGGGGACCTTGCACAGCTGGAATTCATCAG 120
    |||||
Db 131671 GGCTACCAAGATGCCAGATGGCAGATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 131730
    |||||

QY 121 GTACCGGCGGAGCTCAGCCRCGGCCATGCGGGGGGAGGCC 164
    |||||
Db 131731 GTA-CTGACTCAGCTCTCTAGATCCCTGTGGCAGGGGAGGCC 131773
    |||||

RESULT 37
RNO230468 Rattus norvegicus gene encoding inducible nitric oxide synthase,
LOCUS exon 8.
DEFINITION Rattus norvegicus gene encoding inducible nitric oxide synthase,
ACCESSION AJ230468
VERSION 1 GI:5305139
KEYWORDS inducible nitric oxide synthase; iNOS gene.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Keinanen,R., Vartiainen,N. and Koistinaho,J.
TITLE Molecular cloning and characterization of the rat inducible nitric
JOURNAL oxide synthase (iNOS) gene
PUBMED Gene 234 (2), 297-305 (1999)
REFERENCE 2 (bases 1 to 163)
AUTHORS Keinanen,R.A.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1998) Keinanen R.A., A.I. Virtanen Institute,
University of Kuopio, P.O. Box 1627, FIN-70211 Kuopio, Finland
FEATURES
    Location/Qualifiers
        1..163
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            /number=7
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            /genes="iNOS"
        exon 16..157
            /genes="iNOS"
            /product="inducible nitric oxide synthase"
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            /usedin=AJ230462:iNOS_CDS
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ORIGIN
Query Match      38.1%; Score 98.4; DB 9; Length 163;
Best Local Similarity 87.1%; Pred. No. 2.2e-12;

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Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGATGCTCAGCTCATCGGTATGCT 60
    |||||
Db 38 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGATGCTCAGCTCATCGGTATGCT 97
    |||||

QY 61 GGCTACCAAGATGCCAGATGGCAGATCAGAGGGGACCTTGCACAGCTGGAATTCATCAG 120
    |||||
Db 98 GGCTACCAAGATGCCAGATGGCAGATCAGAGGGGATGCTGCCACCTTGGAGTTCACCCAG 157
    |||||

QY 121 GTAC 124
    |||||
Db 158 GTAC 161
    |||||

RESULT 38
AC105495_0
WPCOMMENT
Sequence split into 5 fragments LOCUS AC105495 Accession AC105495
Fragment Name Begin End
AC105495_0 1 110000
AC105495_1 100001 210000
AC105495_2 200001 310000
AC105495_3 300001 410000
AC105495_4 400001 430182
LOCUS AC105495 430182 bp DNA linear HTG 11-OCT-2002
DEFINITION Rattus norvegicus clone CH230-216J16, WORKING DRAFT SEQUENCE, 11
unordered pieces.
ACCESSION AC105495
VERSION AC105495.5 GI:23603886
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 430182)
AUTHORS Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C.,Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Geбреgeorgis,E., Geer,K., Gill,R., Grady,M., Hamilton,C., Hamilton,K.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,B., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
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Mahoney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwokedeme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,

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Rives, C., Rodkey, T., Rojas, A., Rose, M., Ruiz, R., Ruiz, S. J.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sibson, I., Sittler, C. D., Smajls, D.,
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 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstock, G. and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 430182)
 Worley, K. C.
 Direct Submission
 Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 430182)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (11-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 9, 2002 this sequence version replaced gi:21736362.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GNBL
 Center clone name: CH230-216J16
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 252209 bases at least Q40
 Consensus quality: 254267 bases at least Q30
 Consensus quality: 255370 bases at least Q20
 Estimated insert size: 257492; sum-of-contigs estimation
 Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 ----- NOTE: This sequence may represent more than one clone.
 ----- NOTE: This is a 'working draft' sequence. It currently
 consists of 11 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 412811: contig of 412811 bp in length
 412812 412911: gap of unknown length
 412912 413928: contig of 1017 bp in length
 413929 414028: gap of unknown length
 414029 415313: contig of 1285 bp in length
 415314 415413: gap of unknown length

415414 417240: contig of 1827 bp in length
 417241 417340: gap of unknown length
 418441 418441: contig of 1101 bp in length
 418442 418442: gap of unknown length
 419681 419681: contig of 1140 bp in length
 419781 419781: gap of unknown length
 421092 421092: contig of 1311 bp in length
 421192 421192: gap of unknown length
 422330 422330: contig of 1038 bp in length
 422331 422331: gap of unknown length
 423751 423751: contig of 1421 bp in length
 423851 423851: gap of unknown length
 423852 423852: contig of 2130 bp in length
 425981 425981: gap of unknown length
 425982 425982: contig of 4101 bp in length.
 430182: contig of 4101 bp in length.

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ORIGIN
 Query Match 38.1%; Score 98.4; DB 14; Length 110000;
 Best Local Similarity 87.1%; Pred. No. 8.1e-13;
 Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 Qy 1 CACCGGAGTGATCGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

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||||| 33717 GCTTACCAGATCCGATGGCAGCATCAGAGGAGGATCTTGGCCACCTTGGAGTTCCACCCAG 33776
||||| 121 GTAC 124
||||| 33777 GTAC 33780

RESULT 39
AC103040/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-22205, WORKING DRAFT SEQUENCE, 2
unordered pieces.
ACCESSION
AC103040
VERSION
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 240200)
Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
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Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
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Nwaokeleneh, O., Okwuonu, G., Olarnpusagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L., L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, I., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIZT
Center clone name: CH230-22205
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 232006 bases at least Q40
Consensus quality: 234013 bases at least Q30
Consensus quality: 235789 bases at least Q20
Estimated insert size: 243219; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4512: contig of 4512 bp in length
* 4513 4612: gap of unknown length
* 4613 240200: contig of 235588 bp in length.
FEATURES
Source
1..240200
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-22205"
1..1367
/note="wgs_end_extension
clone_end:T7"
3072..4512
/note="wgs_end_extension
clone_end:T7"
4513..4612
/estimated_length=unknown
4613..6492

misc_feature
misc_feature
Gap
misc_feature

```

Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished

2 (bases 1 to 240200)

Worley, K. C.

Direct Submission

Submitted (24-NOV-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 240200)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23123790.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature

table.


```

/note="wgs_end_extension
clone_end:T7"
6768..10860
/misc_feature
/note="wgs_end_extension
clone_end:T7"
10673..11460
/misc_feature
/note="clone_boundary
clone_end:T7
site:ECORI
end sequence:BZ091454"
159678..159821
/misc_feature
/note="clone_boundary
clone_end:Sp6
site:ECORI
end sequence:BZ091456"
238896..240200
/misc_feature
/note="wgs_end_extension
clone_end:Sp6"

ORIGIN
Query Match      38.1%; Score 98.4; DB 14; Length 240200;
Best Local Similarity 87.1%; Pred. No. 7.1e-13;
Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCAAGCAGCACTCCGGGTGTGGAACTGCTCAGCTCATCCGCTAGCT 60
Db 86348 CAGCGGAGCGATGGGAGCATGACTCCGGATCTGGAAATCCCAAGCTCATCCGCTAGCT 86289

Qy 61 GGCTACCAGATGCCAGATCGCAGATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 86288 GGCTACCAGATGCCGATGCCAGATCAGAGGGGATCTGCCCACTTGGATTCACCCAG 86229

Qy 121 GTAC 124
Db 86228 GTAC 86225

RESULT 40
AC106421
LOCUS
DEFINITION Rattus norvegicus clone CH230-126J7, *** SEQUENCING IN PROGRESS
***, 23 unordered pieces.
AC106421
VERSION AC106421.5 GI:30581088
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 314746)
Muzny,D,Marie, Metzker,M, Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Chen, Z.,
Chacko, J., Chavez, D., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falle, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Iladun, S., L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Idludun, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuwha, L., Loulseghe, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenan, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villabana, D., Waldron, D., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlaczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 314746)
Worley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 314746)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24819147.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKWN
Center clone name: CH230-126J7
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 286975 bases at least Q40
Consensus quality: 291712 bases at least Q30
Consensus quality: 295672 bases at least Q20
Estimated insert size: 299042; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.

```


* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

* 13317: contig of 13317 bp in length
* 13318: 13317: gap of unknown length
* 13418: 13417: gap of unknown length
* 19665: contig of 6248 bp in length
* 19765: gap of unknown length
* 19766: 19765: gap of unknown length
* 26052: contig of 6287 bp in length
* 26053: 26052: gap of unknown length
* 26152: gap of unknown length
* 30730: contig of 4578 bp in length
* 30830: gap of unknown length
* 30731: 30830: gap of unknown length
* 42290: contig of 11460 bp in length
* 42390: gap of unknown length
* 280945: contig of 238555 bp in length
* 280946: 280945: gap of unknown length
* 281046: 282338: contig of 1293 bp in length
* 282339: 282438: gap of unknown length
* 283540: contig of 1102 bp in length
* 283541: 283640: gap of unknown length
* 283641: 285082: contig of 1442 bp in length
* 285083: 285182: gap of unknown length
* 285183: 286515: contig of 1333 bp in length
* 286516: 286615: gap of unknown length
* 288419: contig of 1804 bp in length
* 288420: 288519: gap of unknown length
* 288520: 289923: contig of 1404 bp in length
* 289924: 290023: gap of unknown length
* 290024: 291134: contig of 1171 bp in length
* 291135: 291294: gap of unknown length
* 292295: 292998: contig of 1704 bp in length
* 293099: 293098: gap of unknown length
* 294673: 294672: contig of 1574 bp in length
* 294773: 294772: gap of unknown length
* 296577: contig of 1805 bp in length
* 296677: gap of unknown length
* 297798: contig of 1121 bp in length
* 297898: gap of unknown length
* 299653: contig of 1755 bp in length
* 299654: 299753: gap of unknown length
* 301958: contig of 2205 bp in length
* 302058: gap of unknown length
* 304173: contig of 2115 bp in length
* 304174: 304273: gap of unknown length
* 304274: 308177: contig of 3904 bp in length
* 308178: 308277: gap of unknown length
* 308278: 311893: contig of 3616 bp in length
* 311894: 311994: gap of unknown length
* 311994: 314746: contig of 2753 bp in length.

```

FEATURES

source

```

1..314746
  /organism="Rattus norvegicus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10116"
  /clone="CH230-126J7"

```

misc_feature

```
11993..13317
```

```
  /note="wgs contig"
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```
13318..13417
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```
  /estimated_length=unknown
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```
19666..19765
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  /estimated_length=unknown
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```
24770..26052
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  /note="wgs contig"
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```
26053..26152
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  /estimated_length=unknown
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30731..30830
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  /estimated_length=unknown
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36779..38210
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  /note="wgs contig"
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misc_feature

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41173..42290
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```
  /note="wgs contig"
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```
42291..42390
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  /estimated_length=unknown
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```
42391..44327
```

```
  /note="wgs contig"
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```
231963..232756
```

```
  /note="clone boundary
```

```
clone end:T7
```

```
site:EcoRI
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```
end sequence:BH360214"
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```
276085..277158
```

```
  /note="wgs end_extension
```

```
clone end:T7"
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```
278803..280945
```

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  /note="wgs end_extension
```

```
clone end:T7"
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```
280946..281045
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  /estimated_length=unknown
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282339..282438
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  /estimated_length=unknown
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  /estimated_length=unknown
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```
Query Match 38.1%; Score 98.4; DB 14; Length 314746;
```

```
Best Local Similarity 87.1%; Pred. No. 6.9e-13; Indels 0; Gaps 0;
```

```
Matches 108; Conservative 0; Mismatches 16;
```

```
Qy 1 CAGCGAGTGTGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
```

```
Db 20746 CAGCGAGCGATGGGAGCATGACTTCGGGATCTGGAATTCACGCTCATCGCTACGCT 20805
```

```
Qy 61 GGCTACCAAGATGCCAGATGGGAGCATGAGAGGGGACCTGCCAAGTGGGAATTCATCTCAG 120
```

```
Db 20806 GGCTACCAAGATGCCAGATGGGAGCATGAGAGGGGATCTGCCACCTTGGAGTTTACCCAG 20865
```

```
Qy 121 GTAC 124
```

```
Db 20866 GTAC 20869
```

```
Search completed: December 13, 2005, 17:08:45
```

```
Job time : 2148 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 14:11:49 ; Search time 473 Seconds

(without alignments)
3635.287 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 caggcgatgatggcaagca.....ttgtcccccagctgtgcac 258

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	258	14	ADZ75764 Human ind
2	120.4	46.7	1152	4	Aah78096 Nucleotid
3	120.4	46.7	3462	4	Aah78095 Nucleotid
4	120.4	46.7	3462	14	ADV42931 Human psy
5	120.4	46.7	3855	8	ABX76286 Lung canc
6	120.4	46.7	3855	9	ADA09713 Human nit
7	120.4	46.7	3855	13	ACF87485 Human SIR
8	120.4	46.7	3928	13	ACN42845 Human dia
9	120.4	46.7	3946	4	AAC67035 Human ind
10	120.4	46.7	4062	2	AAX08434 Inducible
11	120.4	46.7	4062	10	ACA56880 Human sig
12	120.4	46.7	4062	12	ADI56676 Human pol
13	120.4	46.7	4062	12	ADJ74786 Marker ge
14	120.4	46.7	4062	12	ADJ74903 Marker ge
15	120.4	46.7	4070	2	AAT98199 Human ind
16	120.4	46.7	4133	13	ADQ38958 Human SNP
17	120.4	46.7	4145	2	AAQ66914 Sequence
18	120.4	46.7	4145	2	AAT10115 Nitric ox
19	120.4	46.7	4145	3	AAA34818 Human ade

20	120.4	46.7	4145	3	AAF20940	Aaf20940 Human ind
21	120.4	46.7	4145	4	AAH47966	Aah47966 Mouse ind
22	120.4	46.7	4145	4	AAH47959	Aah47959 Human ind
23	120.4	46.7	4145	10	ABZ96634	Abz96634 Human ind
24	120.4	46.7	4145	11	ABD19732	Abd19732 Human ind
25	120.4	46.7	4164	2	AAQ77700	Aaq77700 Nitric-ox
26	120.4	46.7	4164	11	ADI32081	Adi32081 Human CDN
27	120.4	46.7	4164	13	ADS84148	Ads84148 Human lym
28	120.4	46.7	4221	13	ADQ38959	Adq38959 Human SNP
29	120.4	46.7	4221	14	ABE69128	Ab669128 Human mod
30	120.4	46.7	4277	13	ACN42844	Acn42844 Human dia
31	120.4	46.7	4278	13	ACN42843	Acn42843 Human dia
32	120.4	46.7	8222	3	AAF21450	Aaf21450 Human ind
33	120.4	46.7	8222	10	ABZ97144	Abz97144 Human nuc
34	120.4	46.7	8222	11	ABD19730	Abd19730 Human nuc
35	120.4	46.7	9513	3	AAA34820	Aaa34820 Human ade
36	120.4	46.7	9513	3	AAF20942	Aaf20942 Human low
37	120.4	46.7	9513	10	ABZ96636	Abz96636 Human nuc
38	120.4	46.7	9513	11	ABD20500	Abd20500 Human pul
39	120.4	46.7	35384	3	AAF21436	Aaf21436 Human enz
40	120.4	46.7	35459	10	ABZ97130	Abz97130 Human nuc
41	120.4	46.7	35459	11	ABD17969	Abd17969 Human enz
42	118.8	46.0	4150	4	AAC67036	Aac67036 Human ind
43	118.8	46.0	4150	13	ADS88001	Ads88001 Tumour tr
44	94.8	36.7	1033	2	AAQ79418	Aaq79418 Rat pancr
45	94.8	36.7	3530	2	AAQ79423	Aaq79423 Rat induc

ALIGNMENTS

RESULT 1

ADZ75764

ID ADZ75764 standard; DNA; 258 BP.

XX

AC ADZ75764;

XX

DT 28-JUL-2005 (first entry)

XX

DE Human inducible nitric oxide synthase gene exon 7 SEQ ID NO:1.

XX

KW ds; gene; high altitude pulmonary edema; pulmonary edema;

KW respiratory-gen.; respiratory disease; SNP detection; allelic variation;

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Variation

FT 142

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX

PN US2005106573-A1.

XX

PD 19-MAY-2005.

XX

PF 13-NOV-2003; 2003US-00713137.

XX

PR 13-NOV-2003; 2003US-00713137.

XX

PA (COUN-) COUNCIL SCI & IND RES INDIA.

XX

PI Pasha AQM, Ahsan A;

XX

DR WPI; 2005-384299/39.

XX

PT Detecting predisposition to high altitude pulmonary edema (HAPE) by amplifying intron 7 of human inducible nitric oxide synthase gene, and predicting and analyzing differences in the distribution of allelic variants.

XX

PS Claim 1; SEQ ID NO 1; 13pp; English.

XX

CC The invention relates to a novel method for detecting predisposition to
 CC high altitude pulmonary edema (HAPE). The method comprises amplifying
 CC intron 7 of the human inducible nitric oxide synthase (iNOS) gene
 CC (ADZ75764) by designing and synthesizing forward and reverse
 CC oligonucleotide primers (ADZ75765+ADZ75766), and predicting and
 CC statistically analyzing differences in the distribution of the allelic
 CC variants in the populations, where GG genotype at 19480 position are at
 CC low risk of HAPE, and AA genotype at 19480 position are at high risk of
 CC HAPE. The present sequence represents exon 7 of the human iNOS gene.
 XX
 SQ Sequence 258 BP; 52 A; 80 C; 84 G; 41 T; 0 U; 1 Other;

Query Match 99.8%; Score 257.6; DB 14; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.3e-63;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 QY 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
 DB 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
 QY 121 GTACCCGCGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGTGGTGAGCGAGTG 180
 DB 121 GTACCCGCGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGTGGTGAGCGAGTG 180
 QY 181 ACAGAGTGGAGCCAGAGGAGACACGCGAGCCCGGGCTTACAGACTCACAGGGCCCGTCTT 240
 DB 181 ACAGAGTGGAGCCAGAGGAGACACGCGAGCCCGGGCTTACAGACTCACAGGGCCCGTCTT 240
 QY 241 GTTCCCGCAGCTGTGCATC 258
 DB 241 GTTCCCGCAGCTGTGCATC 258

RESULT 2
 AAH78096
 ID AAH78096 standard; DNA; 1152 BP.
 XX
 AC AAH78096;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a human inducible nitrogen oxide synthase.
 XX
 KW Inducible nitrogen oxide synthase; iNOS; organ rejection;
 KW cerebral infarction; vascular ischemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200166791-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 09-MAR-2001; 2001WO-JP001865.
 XX
 PR 10-MAR-2000; 2000JP-00072480.
 XX
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 PI Ishii Y, Ueda Y, Iwami M, Arakawa H, Notsu Y;
 XX
 DR WPI; 2001-570775/64.
 DR P-PSDB; AAG67464.
 XX
 PT Screening for compounds that inhibit in vitro inducible nitrogen oxide
 PT synthase useful for treating organ rejection, cerebral infarction and
 PT ischemia.
 XX
 PS Claim 11; Page 62; 73pp; Japanese.
 XX

CC The specification describes a method of screening for compounds that
 CC inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The
 CC method comprises contacting the iNOS monomer with a candidate compound,
 CC and selecting those compounds that bind to it. As dimerisation of iNOS is
 CC the final step of the acquisition of the iNOS enzymatic activity, iNOS
 CC inhibitor compounds can be quickly and efficiently screened. The
 CC inhibitors are useful for treatment and prevention of organ rejection,
 CC cerebral infarction and vascular ischemia. The present sequence encodes a
 CC human iNOS
 XX
 SQ Sequence 1152 BP; 275 A; 326 C; 322 G; 229 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 1152;
 Best Local Similarity 99.2%; Pred. No. 2.6e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 379 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 438
 QY 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
 DB 439 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 498
 QY 121 GT 122
 DB 499 CT 500

RESULT 3
 AAH78095
 ID AAH78095 standard; DNA; 3462 BP.
 XX
 AC AAH78095;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of a human polypeptide.
 XX
 KW Inducible nitrogen oxide synthase; iNOS; organ rejection;
 KW cerebral infarction; vascular ischemia; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3462
 FT /*tag= a
 XX
 PN WO200166791-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 09-MAR-2001; 2001WO-JP001865.
 XX
 PR 10-MAR-2000; 2000JP-00072480.
 XX
 PA (FUJI) FUJISAWA PHARM CO LTD.
 XX
 PI Ishii Y, Ueda Y, Iwami M, Arakawa H, Notsu Y;
 XX
 DR WPI; 2001-570775/64.
 DR P-PSDB; AAG67463.
 XX
 PT Screening for compounds that inhibit in vitro inducible nitrogen oxide
 PT synthase useful for treating organ rejection, cerebral infarction and
 PT ischemia.
 XX
 PS Disclosure; Page 50-53; 73pp; Japanese.
 XX
 CC The specification describes a method of screening for compounds that
 CC inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The
 CC method comprises contacting the iNOS monomer with a candidate compound,
 CC and selecting those compounds that bind to it. As dimerisation of iNOS is

CC the final step of the acquisition of the iNOS enzymatic activity, iNOS
 CC inhibitor compounds can be quickly and efficiently screened. The
 CC inhibitors are useful for treatment and prevention of organ rejection,
 CC cerebral infarction and vascular ischemia. The present sequence was used
 CC in the course of the invention
 XX
 SQ Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 3462;
 Best Local Similarity 99.2%; Pred. No. 3.3e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCCGCTATGCT 60
 |||||
 Db 745 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCCGCTATGCT 804
 |||||
 QY 61 GGTACACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACTGGAATTCACCTCAG 120
 |||||
 Db 805 GGCTACACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACTGGAATTCACCTCAG 864
 |||||
 QY 121 GT 122
 ||
 Db 865 CT 866

RESULT 4
 ADV42931
 ID ADV42931 standard; cDNA; 3462 BP.
 XX
 AC ADV42931;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Human psychoneuroendocrine-immune expressed sequence tag SEQ ID NO 559.
 XX
 KW microarray; psychoneuroendocrine-immune; chronic fatigue;
 KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
 KW cancer; neoplasm; infection; expressed sequence tag; ss.
 XX
 OS Homo sapiens.

XX
 PN W02004108899-A2.
 XX
 PD 16-DEC-2004.
 XX
 PF 04-JUN-2004; 2004WO-US017686.
 XX
 PR 04-JUN-2003; 2003US-0475915P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Nicholson A, Vernon SD;
 XX
 DR WPI; 2005-031682/03.
 XX

PT New microarray comprising probes for genes involved in
 PT psychoneuroendocrine-immune (PNI) activity, useful in diagnosing a
 PT condition associated with PNI activity, e.g., inflammatory or infectious
 PT diseases.

XX
 PS Claim 1; SEQ ID NO 559; 254pp; English.
 XX
 CC The invention relates to a new microarray which comprises probes for
 CC genes involved in psychoneuroendocrine-immune (PNI) activity. The
 CC microarray is useful in diagnosing a condition associated with PNI
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 CC cancer and infection. The present sequence represents a
 CC psychoneuroendocrine-immune gene expressed sequence tag. Note the
 CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
 CC SEQ ID NO 1829 are provided.

XX Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 14; Length 3462;
 Best Local Similarity 99.2%; Pred. No. 3.3e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCCGCTATGCT 60
 |||||
 Db 745 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCCGCTATGCT 804
 |||||
 QY 61 GGTACACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACTGGAATTCACCTCAG 120
 |||||
 Db 805 GGCTACACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACTGGAATTCACCTCAG 864
 |||||
 QY 121 GT 122
 ||
 Db 865 CT 866

RESULT 5
 ABX76286
 ID ABX76286 standard; DNA; 3855 BP.
 XX
 AC ABX76286;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #150.

XX Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.

XX
 PN W0200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 DR WPI; 2003-093161/08.
 DR P-PSDB; ABU56557.

PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.

XX Claim 22; Page 301-302; 453pp; English.

XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are
 CC disclosed within the specification, however, these have not been taken
 CC into account during indexing due to inconsistencies in application and
 CC format
 XX
 SQ Sequence 3855 BP; 897 A; 1134 C; 1065 G; 759 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 13; Length 3855;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24; Mismatches 0; Indels 0; Gaps 0;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 60
 DB 939 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 998
 QY 61 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCAACGTGGAATTCATCTAG 120
 DB 999 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCAACGTGGAATTCATCTAG 1058
 QY 121 GT 122
 DB 1059 CT 1060
 RESULT 8
 ACN42845
 ID ACN42845 standard; cDNA; 3928 BP.
 XX
 AC ACN42845;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1720.
 XX
 KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
 KW dithp.
 KW
 XX Homo sapiens.
 OS
 XX WO2004023973-A2.
 PN
 XX 25-MAR-2004.
 PD
 XX 12-SEP-2003; 2003WO-US028227.
 PF
 XX 12-SEP-2002; 2002US-0410259P.
 PR
 XX 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Bider LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patary S, Shi X, Suarez CJ;
 XX
 DR WPI; 2004-329368/30.
 DR P-PSDB; ABM84193.
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 XX Claim 1; Page; 190pp; English.
 PS
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp polynucleotide of
 CC the invention. Note: The sequence data for this patent is not represented
 CC in the printed specification, but was obtained in electronic format
 CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 3928 BP; 928 A; 1151 C; 1086 G; 763 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 13; Length 3928;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24; Mismatches 0; Indels 0; Gaps 0;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 60
 DB 998 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 1057
 QY 61 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCAACGTGGAATTCATCTAG 120
 DB 1058 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCAACGTGGAATTCATCTAG 1117
 QY 121 GT 122
 DB 1118 CT 1119
 RESULT 9
 AAC67035
 ID AAC67035 standard; DNA; 3946 BP.
 XX
 AC AAC67035;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Human inducible nitric oxide synthase coding sequence #1.
 XX
 KW Human; influenza virus; antisense; inducible nitric oxide synthase; iNOS;
 KW ds.
 XX
 OS Homo sapiens.
 OS
 XX WO200078946-A2.
 PN
 XX 28-DEC-2000.
 PD
 XX 19-JUN-2000; 2000WO-US016810.
 PF
 XX 17-JUN-1999; 99US-0139479P.
 PR
 XX (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
 PA
 XX Keller ET, Gravenstein S, Hall DM;
 PI WPI; 2001-102720/11.
 DR
 XX
 XX Treating viral influenza with antisense oligonucleotides that hybridize
 PT with inducible nitric oxide synthase mRNA and inhibit synthesis of the
 PT enzyme, reducing the production of nitric oxide in lungs.
 XX
 XX Disclosure; Fig 1; 21pp; English.
 PS
 XX The present invention provides a novel method of treating influenza virus
 CC infection by administering an antisense oligonucleotide directed at the
 CC human inducible nitric oxide synthase (iNOS) mRNA. This is useful in
 CC preventing the symptoms of influenza infection
 XX
 SQ Sequence 3946 BP; 918 A; 1149 C; 1073 G; 806 T; 0 U; 0 Other;

```

Query Match      46.7%; Score 120.4; DB 4; Length 3946;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 745 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCACCTCAG 120
DB 805 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCACCTCAG 864

QY 121 GT 122
DB 865 CT 866

RESULT 10
AAX08434
ID AAX08434 standard; DNA; 4062 BP.
XX AC AAX08434;
XX 28-JUN-1999 (first entry)
XX Inducible nitric oxide synthase gene.
XX Manganese containing superoxide dismutase; MnSOD; IDDM;
XX diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;
XX fatty acids; lipotoxic; cytotoxic; cytokine; osteoporosis;
XX inflammatory disease; autoimmune disease; neurodegenerative disease; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 106..3567
XX /*tag= a
XX /product= "Nitric oxide synthase"
XX WO9906059-A2.
XX 11-FEB-1999.
XX 30-JUL-1998; 98WO-US015781.
XX 30-JUL-1997; 97US-0055092P.
XX 03-MAR-1998; 98US-0076676P.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX (BETA-) BETAGENE INC.
XX Hohmeier H, Thigpen A, Clark SA, Newgard CB, Unger RH;
XX Shimabukuro M, Koyama K, Ohneda M, Lee Y;
XX WPI; 1999-153448/13.
XX P-PSDB; AAW96322.
XX Protection of mammalian cells against immunotoxicity or lipotoxicity -
XX used for treating, e.g. diabetes, obesity, wasting syndromes,
XX osteoporosis, inflammatory diseases, autoimmune diseases or
XX neurodegenerative diseases.
XX Disclosure; Page 244-247; 253pp; English.
XX Inhibition of cytokine mediated immunotoxicity of cells can be achieved
XX by blocking free radical production or the accumulation of free radicals
XX in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can
XX be achieved by blocking nitric oxide (NO) production in a pancreatic
XX beta cell and by providing a composition comprising an agent that reduces
XX levels of fatty acids in the cells and protects beta-cells of the subject
XX against lipid-mediated cell death. Cells can also be protected against
XX nitric oxide mediated cytotoxicity by introducing into the cell an

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CC antioxidant agent. The methods can be used for protecting cells against
CC immunotoxicity mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF
CC alpha, TNF beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14,
CC IL-17, granulocyte-macrophage colony stimulating factor or monocyte
CC chemottractant protein-1. The methods can be used for the treatment of
CC e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting
CC syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune
CC diseases, or neurodegenerative diseases
XX
SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
Query Match      46.7%; Score 120.4; DB 2; Length 4062;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 850 CAGCGGAGTGATGCCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCACCTCAG 120
DB 910 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCACCTCAG 969

QY 121 GT 122
DB 970 CT 971

RESULT 11
ACA56880
ID ACA56880 standard; cDNA; 4062 BP.
XX AC ACA56880;
XX 06-JUN-2003 (first entry)
XX Human signalling pathway polynucleotide probe SEQ ID NO 1478.
XX Human; probe; ss; array element; Parkinson's disease;
XX signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX Homo sapiens.
XX US6500938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides.
XX Claim 1; SEQ ID NO 1478; 65pp; English.
XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX forensics and pharmacogenomics. The microarray is also useful for

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CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signaling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: the sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
 XX
 SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 10; Length 4062;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
 DB 850 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 909
 QY 61 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
 DB 910 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
 QY 121 GT 122
 DB 970 CT 971
 RESULT 12
 ADI56676
 ID ADI56676 standard; DNA; 4062 BP.
 AC ADI56676;
 DT 22-APR-2004 (first entry)
 DE Human polynucleotide probe #1478.
 XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
 KW effector-like polypeptide; cancer; immunopathology; neuropathology;
 KW drug development; toxicology; carcinogenicity;
 KW signalling pathway polypeptide; adrenal gland; bladder; bone;
 KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
 KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
 KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
 XX
 OS Homo sapiens.
 XX
 XX US2004010136-A1.
 XX
 PD 15-JAN-2004.
 XX
 XX 26-NOV-2002; 2002US-00305720.
 XX
 XX 30-JAN-1998; 98US-00016434.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Au-Young J, Seilhamer JJ;
 XX WPI; 2004-090520/09.
 XX
 XX New composition comprising polynucleotide probes, useful as array
 PT elements in a microarray for monitoring the expression of target
 PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
 PT fragments.
 XX
 XX Claim 6; SEQ ID NO 1478; 73pp; English.

XX The invention relates to a composition of polynucleotide probes
 CC comprising first polynucleotide probes comprising at least a portion of a
 CC gene encoding a receptor-like polypeptide, second polynucleotide probes
 CC comprising at least a portion of a gene encoding a transducing
 CC polypeptide and third polynucleotide probes comprising at least a portion
 CC of a gene encoding an effector-like polypeptide. The probes of the
 CC composition are useful as array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray is useful in the
 CC diagnosis and treatment of cancer, an immunopathology or a
 CC neuropathology. It can also be used for drug discovery and development,
 CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
 CC Microarrays can also be used for monitoring the progression of diseases
 CC that may be associated with the altered expression of signalling pathway
 CC polypeptides. The composition can also be used to purify a subpopulation
 CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
 CC is also useful for the diagnosis and treatment of cancer e.g. cancers of
 CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
 CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
 CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
 CC epilepsy, Alzheimer's disease or depression. This sequence represents a
 CC human polynucleotide probe of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 12; Length 4062;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
 DB 850 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 909
 QY 61 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
 DB 910 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
 QY 121 GT 122
 DB 970 CT 971
 RESULT 13
 ADJ74786
 ID ADJ74786 standard; DNA; 4062 BP.
 XX ADJ74786;
 XX 20-MAY-2004 (first entry)
 DT
 XX
 XX Marker gene SEQ ID NO:38.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker gene; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX EP1394274-A2.
 XX
 XX 03-MAR-2004.
 XX
 XX 04-AUG-2003; 2003EP-00254857.
 XX
 XX 06-AUG-2002; 2002JP-00229312.
 XX 20-MAR-2003; 2003JP-00077212.
 XX
 XX (GENO-) GENOX RES INC.
 XX
 XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by

XX comparing the expression level of a marker gene in a biological sample

XX from a subject with the expression level of the gene in a sample from a

XX healthy subject.

XX Claim 1; SEQ ID NO 38; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma

XX or chronic obstructive pulmonary disease. The method comprises

XX determining the expression level of a marker gene in a biological sample

XX from a subject, comparing the expression level determined with the

XX expression level of the marker gene in a biological sample from a healthy

XX subject, and judging whether the subject has bronchial asthma or chronic

XX obstructive pulmonary disease. The marker gene comprises: (a) a group of

XX genes (S1) whose expression levels increase when respiratory epithelial

XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)

XX whose expression levels decrease when respiratory epithelial cells are

XX stimulated with interleukin-13. Also described: (1) a reagent (I) for

XX testing for bronchial asthma or chronic obstructive pulmonary disease;

XX (2) a kit for screening for a candidate compound for a therapeutic agent

XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

XX an animal model for bronchial asthma or chronic obstructive pulmonary

XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

XX method for producing an animal model for bronchial asthma or chronic

XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial

XX asthma or chronic obstructive pulmonary disease, comprising the compound,

XX a marker gene or an antisense nucleic acid corresponding to a portion of

XX the marker gene, a ribozyme, a polynucleotide that suppresses the

XX expression of the gene through an RNAi effect or an antibody recognising

XX a protein encoded by a marker gene; and (7) a DNA chip for testing for

XX bronchial asthma or a chronic obstructive pulmonary disease, on which a

XX probe has been immobilised to assay a marker gene. (I) has respiratory

XX and antiasthmatic activities, and can be used in gene therapy. The method

XX is useful for testing for or screening for a therapeutic agent for

XX bronchial asthma or chronic obstructive pulmonary disease. The present

XX sequence is used in the exemplification of the present invention.

SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 12; Length 4062;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

DB 850 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120

DB 910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 969

QY 121 GT 122

DB 970 CT 971

RESULT 14

ADJ74903

ID ADJ74903 standard; DNA; 4062 BP.

XX

AC ADJ74903;

XX

DT 20-MAY-2004 (first entry)

XX

DE Marker gene SEQ ID NO:155.

XX

KW bronchial asthma; chronic obstructive pulmonary disease;

KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

KW gene therapy; marker gene; gene; ds.

XX

OS Homo sapiens.

XX

PN EP1394274-A2.

XX

PD 03-MAR-2004.

XX

XX 04-AUG-2003; 2003EP-00254857.

XX

XX 06-AUG-2002; 2002JP-00229312.

PR

PR 20-MAR-2003; 2003JP-00077212.

XX

XX (GENO-) GENOX RES INC.

XX

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by

XX comparing the expression level of a marker gene in a biological sample

XX from a subject with the expression level of the gene in a sample from a

XX healthy subject.

XX Claim 1; SEQ ID NO 155; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma

XX or chronic obstructive pulmonary disease. The method comprises

XX determining the expression level of a marker gene in a biological sample

XX from a subject, comparing the expression level determined with the

XX expression level of the marker gene in a biological sample from a healthy

XX subject, and judging whether the subject has bronchial asthma or chronic

XX obstructive pulmonary disease. The marker gene comprises: (a) a group of

XX genes (S1) whose expression levels increase when respiratory epithelial

XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)

XX whose expression levels decrease when respiratory epithelial cells are

XX stimulated with interleukin-13. Also described: (1) a reagent (I) for

XX testing for bronchial asthma or chronic obstructive pulmonary disease;

XX (2) a kit for screening for a candidate compound for a therapeutic agent

XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

XX an animal model for bronchial asthma or chronic obstructive pulmonary

XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

XX method for producing an animal model for bronchial asthma or chronic

XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial

XX asthma or chronic obstructive pulmonary disease, comprising the compound,

XX a marker gene or an antisense nucleic acid corresponding to a portion of

XX the marker gene, a ribozyme, a polynucleotide that suppresses the

XX expression of the gene through an RNAi effect or an antibody recognising

XX a protein encoded by a marker gene; and (7) a DNA chip for testing for

XX bronchial asthma or a chronic obstructive pulmonary disease, on which a

XX probe has been immobilised to assay a marker gene. (I) has respiratory

XX and antiasthmatic activities, and can be used in gene therapy. The method

XX is useful for testing for or screening for a therapeutic agent for

XX bronchial asthma or chronic obstructive pulmonary disease. The present

XX sequence is used in the exemplification of the present invention.

SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 12; Length 4062;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

DB 850 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120

DB 910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 969

QY 121 GT 122

DB 970 CT 971

RESULT 15
AAT98199
ID AAT98199 standard; cDNA; 4070 BP.
XX AC AAT98199;
XX DT 11-MAY-1998 (first entry)
XX DE Human inducible nitric oxide synthetase cDNA.
XX KW Nitric oxide synthetase; NOS; iNOS; HPI NOS; human; erectile dysfunction;
XX KW impotence; gene therapy; corpora cavernosa; relaxant; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 197..3658
XX FT /*tag= a
XX PN WO9742965-A1.
XX PD 20-NOV-1997.
XX PE 09-MAY-1997; 97WO-US007643.
XX PR 10-MAY-1996; 96US-0017373P.
XX PA (GONZ/) GONZALEZ-CADAVID N F.
XX PA (RAJF/) RAJFER J.
XX PI Gonzalez-Cadavid NF, Rajfer J;
XX DR WPI; 1998-008577/01.
XX DR P-PSDB; AAW36113.
XX PT Treatment of erectile dysfunction - by introducing an agent into penile
XX PT tissue, particularly for inducing cavernosal smooth muscle relaxation or
XX PT increasing NOS levels.
XX PS Claim 14; Page 35-38; 53pp; English.
XX CC This cDNA sequence includes a coding region for human penis inducible
XX CC nitric oxide synthetase (HPI NOS) (see AAW36113). It was isolated by
XX CC reverse transcription of mRNA from human penile smooth muscle cells with
XX CC INOS antisense primers, combined with PCR amplification of the resulting
XX CC cDNA fragments. The invention is directed to a method of treating
XX CC erectile dysfunction in a patient by providing an agent capable of
XX CC treating erectile dysfunction, and introducing an effective amount of the
XX CC agent into the penile tissue of the patient. Preferably, the agent
XX CC induces cavernosal smooth muscle relaxation, and/or produces an increase
XX CC in the level of NOS in tissue. Preferably, the NOS is iNOS, and the agent
XX CC is introduced into the corpora cavernosa of the penis. The agent is
XX CC preferably an NOS inducer, an NOS protein such as HPI NOS, a cDNA encoding
XX CC an NOS such as HPI NOS, or cDNA-transformed penile cells, especially
XX CC corpora cavernosa cells
XX SQ Sequence 4070 BP; 947 A; 1197 C; 1112 G; 814 T; 0 U; 0 Other;
Query Match 46.7%; Score 120.4; DB 2; Length 4070;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
941 CAGCGGAGTGATGGCAAGCAGACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1000
QY 61 GGCTACCATGATCCAGATGGCAGATCAGAGGGGACCTGCCACGTGGGAATTCCTCAG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1001 GGCTACCATGATCCAGATGGCAGATCAGAGGGGACCTGCCACGTGGGAATTCCTCAG 1060
QY 121 GT 122
DB 1061 CT 1062

RESULT 16
ADQ38958
ID ADQ38958 standard; DNA; 4133 BP.
XX AC ADQ38958;
XX DT 18-NOV-2004 (first entry)
XX DE Human SNP containing myocardial infarction-associated gene, SEQ ID 621.
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX KW cardiant; gene therapy; human; gene; ds.
XX OS Homo sapiens.
XX PN WO2004058052-A2.
XX PD 15-JUL-2004.
XX PF 22-DEC-2003; 2003WO-US040978.
XX PR 20-DEC-2002; 2002US-0434778P.
XX PR 10-MAR-2003; 2003US-0453135P.
XX PR 30-APR-2003; 2003US-0466412P.
XX PR 23-SEP-2003; 2003US-0504955P.
XX PA (APPL-) APPLERA CORP.
XX PI Cargill M, Devlin JJ, Iakubova O;
XX DR WPI; 2004-533949/51.
XX DR P-PSDB; ADQ39786.
XX PT Identifying an individual who has an altered risk for developing
XX PT myocardial infarction by detecting a single nucleotide polymorphism in
XX PT the individual's nucleic acids.
XX PS Claim 7; SEQ ID NO 621; 145pp; English.
XX CC The invention relates to a novel method for identifying an individual who
XX CC has an altered risk for developing myocardial infarction. The method
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
XX CC the nucleotide sequences given in the specification in the individual's
XX CC nucleic acids, where the presence of the SNP is correlated with an
XX CC altered risk for myocardial infarction in the individual. The invention
XX CC further comprises: an isolated nucleic acid molecule comprising at least
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
XX CC the specification or its complement and encoding any one of the amino
XX CC acid sequences given in the specification; an isolated polypeptide
XX CC comprising an amino acid sequence given in the specification; an antibody
XX CC that specifically binds to the polypeptide or its antigen-binding
XX CC fragment; an amplified polynucleotide containing an SNP given in the
XX CC specification and which is between about 16 and 1000 nucleotides in
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
XX CC method for identifying an agent useful in treating or preventing
XX CC myocardial infarction. The novel detection method has cardiant activity.
XX CC The nucleic acids of the invention may be used in gene therapy. The
XX CC method is useful in identifying an individual who has an increased or
XX CC decreased risk for developing myocardial infarction and for preparing a
XX CC composition for treating or preventing myocardial infarction. This
XX CC polynucleotide sequence represents a human myocardial infarction-
XX CC associated gene containing one or more SNPs of the invention. Note: This
XX CC sequence was not shown in the specification. The sequence has come from
XX CC an electronic sequence listing downloaded from the WIPO website.
XX SQ Sequence 4133 BP; 960 A; 1198 C; 1118 G; 840 T; 0 U; 17 Other;
Query Match 46.7%; Score 120.4; DB 13; Length 4133;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 Db 939 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
 Qy 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120
 Db 999 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1058
 Qy 121 GT 122
 Db 1059 CT 1060

RESULT 17
 ID AAQ66914 standard; cDNA; 4145 BP.
 AC AAQ66914;
 XX
 DT 25-MAR-2003 (revised)
 DT 28-DEC-1994 (first entry)
 XX
 DE Sequence of the cDNA clone for human hepatocyte inducible nitric oxide synthase.
 DE
 XX Nitric oxide synthase; hepatocyte; hypotensive shock; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 207..3668
 FT /*tag= a
 FT
 XX
 FN WO9412645-A2.
 XX
 PD 09-JUN-1994.
 XX
 PF 23-NOV-1993; 93WO-US011401.
 XX
 PR 25-NOV-1992; 92US-00981344.
 XX
 XX (UYPI-) UNIV PITTSBURGH.
 XX
 PI Billiar TR, Nussler AK, Geller DA, Simmons RL;
 XX
 DR WPI; 1994-200273/24.
 DR P-PSDB; AAR55764.
 XX
 PT cDNA clone encoding human inducible nitric oxide synthase - used to prevent the hypotensive shock seen with sepsis.
 PT
 PS Claim 23; Fig 1; 53pp; English.
 XX
 CC AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA clone PHINOS from lambda Zap II cDNA library. The original source was induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in E. coli SOLR (ATCC 69126). The inventors claim a clone with the cDNA sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning and expression of a human tissue nitric oxide synthase cDNA provides a source of the enzyme for therapeutic purposes, for example to prevent the hypotensive shock seen with sepsis. (Updated on 25-MAR-2003 to correct FN field.)
 CC
 XX
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 2; Length 4145;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 Db 939 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
 Qy 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120
 Db 999 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1070
 Qy 121 GT 122
 Db 1071 CT 1072

RESULT 18
 ID AAT10115 standard; cDNA; 4145 BP.
 AC AAT10115;
 XX
 DT 13-MAY-1996 (first entry)
 DT
 XX
 DE Nitric oxide synthase cDNA clone PHINOS.
 DE
 XX Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;
 XX
 KW vascular occlusive disease; cancer; infection; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 207..3668
 FT /*tag= a
 FT
 XX
 FN WO9600006-A1.
 XX
 PD 04-JAN-1996.
 XX
 PF 20-JUN-1995; 95WO-US007849.
 XX
 PR 24-JUN-1994; 94US-00265046.
 XX
 XX (UYPI-) UNIV PITTSBURGH.
 XX
 PI Billiar TR, Tzeng E, Nussler AK, Geller DA, Simmons RL;
 XX
 DR WPI; 1996-068641/07.
 DR P-PSDB; AAR88464.
 XX
 PT Inducible nitric oxide synthase gene - useful in gene therapy to treat, e.g. vascular occlusive disease and cancer.
 PT
 PS Claim 72; Page 53-58; 91pp; English.
 XX
 CC A cDNA clone (AAT10115), designated PHINOS, codes for the human hepatocyte inducible nitric oxide synthase (iNOS = AAR88464). It was obtd. by isolating mRNA from hepatocytes induced in vitro for iNOS biosynthesis, preparing a cDNA library in a phage lambda Zap II vector, and screening with a cross-species iNOS probe. The cDNA can be used to prepare iNOS for therapeutic use. Alternatively, it is used in gene therapy strategies for treatment of vascular occlusive disease associated with atherosclerosis, vascular bypass and diabetes mellitus, tumor cell growth, and microbial infections
 CC
 XX
 SQ Sequence 4145 BP; 968 A; 1205 C; 1124 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 2; Length 4145;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 Db 951 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
 Qy 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120
 Db 1011 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1070

QY 121 GT 122
 Db 1071 CT 1072

RESULT 19
 AAA34818
 ID AAA34818 standard; DNA; 4145 BP.
 XX
 AC AAA34818;
 XX
 XX
 DT 28-JUL-2000 (first entry)
 XX
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2507.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 PF
 XX 03-AUG-1998; 98US-0095212P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 XX Disclosure; Page 664-665; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 3; Length 4145;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAAGCAGACGCTTCGGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60
 Db 951 CAGCGGAGTGATGGCAAGCAGACGCTTCGGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 1010
 QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGCAACGTGGAATTCATCTCAG 120
 Db 1011 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGCAACGTGGAATTCATCTCAG 1070
 QY 121 GT 122
 Db 1071 CT 1072

RESULT 20
 AAF20940
 ID AAF20940 standard; DNA; 4145 BP.
 XX
 AC AAF20940;
 XX
 XX 14-MAR-2001 (first entry)
 DT
 XX
 DE Human inducible nitric oxide synthase polynucleotide fragment #2507.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosstatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Disclosure; Page 254-255; 1592pp; English.
 PS
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytosstatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,

CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF10434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 3; Length 4145;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTATCGCTATGCT 60
 DB 951 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTATCGCTATGCT 1010
 QY 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACGTTGGAATTCACCTCAG 120
 DB 1011 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACGTTGGAATTCACCTCAG 1070
 QY 121 GT 122
 DB 1071 CT 1072
 RESULT 21
 AAH47966
 ID AAH47966 standard; cDNA; 4145 BP.
 XX
 AC AAH47966;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase encoding cDNA 1.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 CDS 207..3668
 FT /*tag= a
 FT /product= "inducible nitric oxide synthase"
 XX
 PN WO200152902-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 15-JAN-2001; 2001WO-US001381.
 XX
 PR 24-JAN-2000; 2000US-00490208.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dean NM, Cowseert LM;

XX WPI; 2001-465340/50.
 DR P-PSDB; AAG64498.
 XX
 PT New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 XX
 PS Example 13; Page 98-103; 144pp; English.
 XX
 CC The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase (Genbank accession number M92649)
 XX
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 4; Length 4145;
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTATCGCTATGCT 60
 DB 951 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTATCGCTATGCT 1010
 QY 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACGTTGGAATTCACCTCAG 120
 DB 1011 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACGTTGGAATTCACCTCAG 1070
 QY 121 GT 122
 DB 1071 CT 1072
 RESULT 22
 AAH47959
 ID AAH47959 standard; cDNA; 4145 BP.
 XX
 AC AAH47959;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Human inducible nitric oxide synthase encoding cDNA 1.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 207..3668
 FT /*tag= a
 FT /product= "inducible nitric oxide synthase"
 XX
 PN WO200152902-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 15-JAN-2001; 2001WO-US001381.
 XX

```
PR 24-JAN-2000; 2000US-00490208.
XX (ISIS-) ISIS PHARM INC.
PA Bennett CP, Dean NM, Cowsert LM;
XX WPI; 2001-465340/50.
DR P-PSDB; AAG64497.
XX
XX New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischemia.
XX
XX Example 13; Page 92-97; 144pp; English.
XX
XX The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridise to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiac
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of
CC human inducible nitric oxide synthase (GenBank accession number L09210)
XX
XX Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 4; Length 4145;
Best Local Similarity 99.2%; Pred.No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCGCGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
DB 951 CAGCGGAGTGATGCGAAGCAGCACTTCGCGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
DB 1011 GGCTACCCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070
QY 121 GT 122
DB 1071 CT 1072
RESULT 23
ABZ96634
ID ABZ96634 standard; DNA; 4145 BP.
XX
XX ABZ96634;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human inducible nitric oxide synthase nucleic acid.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
PR 23-APR-2002; 2002MO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 11876; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 10; Length 4145;
Best Local Similarity 99.2%; Pred.No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCGCGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
DB 951 CAGCGGAGTGATGCGAAGCAGCACTTCGCGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
DB 1011 GGCTACCCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070
QY 121 GT 122
DB 1071 CT 1072
RESULT 24
ABD19732
ID ABD19732 standard; DNA; 4145 BP.
XX
XX ABD19732;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human inducible nitric oxide synthase DNA fragment #3.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
```



```
RESULT 26
AD132081
ID ADI32081 standard; cDNA; 4164 BP.
XX
AC AC
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #1407.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 1407; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 120.4; DB 11; Length 4164;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 27
ADS84148
ID ADS84148 standard; cDNA; 4164 BP.
XX
AC ADS84148;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human lymph node cDNA #1407.
XX
KW ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
OS Homo sapiens.
XX
PN US2004077003-A1.
XX
PD 22-APR-2004.
XX
PF 14-AUG-2003; 2003US-00641643.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2004-387937/36.
XX
PT New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
PS Claim 15; SEQ ID NO 1407; 16pp; English.
XX
CC The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?docID=20040077003).
XX
SQ Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 U; 0 Other;
XX
Query Match 46.7%; Score 120.4; DB 13; Length 4164;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
|||
Db 970 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1029
|||
QY 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTTGGAATTCACCTCAG 120
|||
Db 1030 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTTGGAATTCACCTCAG 1089
|||
QY 121 GT 122
|
Db 1090 CT 1091
||
RESULT 28
ID ADQ38959 standard; DNA; 4221 BP.
AC ADQ38959;
XX
XX
DT 18-NOV-2004 (first entry)
XX
XX Human SNP containing myocardial infarction-associated gene, SEQ ID 622.
XX
XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX WO2004058052-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PA
XX
XX Cargill M, Devlin JJ, Iakoubova O;
PI
XX
XX WPI; 2004-533949/51.
DR P-PSDB; ADQ39787.
DR
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX
XX Claim 7; SEQ ID NO 622; 145pp; English.
PS
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 15 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 4221 BP; 998 A; 1216 C; 1133 G; 857 T; 0 U; 17 Other;
||
Query Match 46.7%; Score 120.4; DB 13; Length 4221;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
||
QY 1 CAGCGGAGTGATGCGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
|||
Db 1009 CAGCGGAGTGATGCGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1068
|||
QY 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTTGGAATTCACCTCAG 120
|||
Db 1069 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTTGGAATTCACCTCAG 1128
|||
QY 121 GT 122
|
Db 1129 CT 1130
||
RESULT 29
ID AEB69128 standard; DNA; 4221 BP.
XX
XX AEB69128;
AC
XX
XX 20-OCT-2005 (first entry)
DT
XX
XX Human modulator of IGFR pathway polynucleotide #5.
DE
XX
XX Screening; insulin growth factor receptor; IGFR; diagnosis; cancer;
KW neoplasm; cytostatic; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX WO2005073723-A1.
XX
XX 11-AUG-2005.
PD
XX
XX 27-JAN-2005; 2005WO-US002638.
XX
XX 28-JAN-2004; 2004US-0539837P.
PR 12-MAR-2004; 2004US-0552634P.
PR 21-JUN-2004; 2004US-0581696P.
XX
XX (EXEL-) EXELIXIS INC.
PA (NICO/) NICOLL M.
XX
XX Nicoll M, Friedman L, Francis-Lang H, Parks A, Shaw KJ, Zhang H;
PI Björke LM, Adamkewicz J, Hitz BC, Lickteig K, Jin Y;
XX
XX WPI; 2005-582573/59.
DR P-PSDB; AEB69188.
DR
XX
XX Identifying a candidate insulin growth factor receptor (IGFR) pathway
PT modulating agents useful for diagnosing or treating, for e.g. cancer;
PT comprises screening for agents that modulate the activity of a modifier
PT of IGFR (MIGFR).
XX
XX Example; SEQ ID NO 5; 334pp; English.
PS
XX
XX The invention relates to a method of identifying a candidate insulin
CC growth factor receptor (IGFR) pathway modulating agent comprising
CC screening for agents that modulate the activity of a modifier of IGFR
CC (MIGFR). The method comprises providing an assay system comprising an
CC MIGFR polypeptide or polynucleotide, contacting the assay system with a
CC test agent under conditions where, but for the presence of the test

CC agent, the system provides a reference activity and detecting a test
CC agent-biased activity of the assay system, where a difference between the
CC test agent-biased activity and the reference activity identifies the test
CC agent as a candidate IGR pathway modulating agent. The invention also
CC relates to methods for modulating an IGR pathway of a cell or in a
CC mammalian cell and a method for diagnosing a disease in a patient. The
CC methods are useful for diagnosing or treating cancer or for identifying
CC modulators of an IGR pathway, which may be utilized as therapeutic
CC targets for disorders associated with defective IGR function, such as
CC cancer. This sequence represents a human modulator of IGR pathway
CC polynucleotide of the invention.

XX Sequence 4221 BP; 1001 A; 1221 C; 1138 G; 861 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 14; Length 4221;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60

DB 1009 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGTCAATCGCTATGCT 1068

QY 61 GCCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTCAG 120

DB 1069 GCCTACCATGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTCAG 1128

QY 121 GT 122

DB 1129 CT 1130

RESULT 30

ACN42844

ID ACN42844 standard; cDNA; 4277 BP.

XX ACN42844;

XX 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1719.

XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;

XX dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RU, Bruns CM, Marjanovic MM, Shen F;

XX Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;

XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patry S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX P-PSDB; ABM84192.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX in diagnosing a condition, disease or disorder associated with human

XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX in gene mapping.

XX Claim 1; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dithp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dithp polynucleotide of
XX the invention. Note: The sequence data for this patent is not represented
XX in the printed specification, but was obtained in electronic format
XX directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 4277 BP; 973 A; 1253 C; 1237 G; 814 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 13; Length 4277;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60

DB 1348 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGTCAATCGCTATGCT 1407

QY 61 GCCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTCAG 120

DB 1408 GCCTACCATGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTCAG 1467

QY 121 GT 122

DB 1468 CT 1469

RESULT 31

ACN42843

ID ACN42843 standard; cDNA; 4278 BP.

XX ACN42843;

XX 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1718.

XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;

XX dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;

XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patry S, Shi X, Suarez CJ;

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XX WPI; 2004-329368/30.
DR P-FSDB; ABM84191.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 1; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 4278 BP; 972 A; 1253 C; 1238 G; 815 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 13; Length 4278;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 1348 CAGCGGAGTGATGCAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1407
Qy 61 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1408 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 1467
Qy 121 GT 122
Db 1468 CT 1469
RESULT 32
AAF21450
ID AAF21450 standard; DNA; 8222 BP.
XX
XX AAF21450;
XX
XX 14-MAR-2001 (first entry)
XX
XX Human inducible nitric oxide synthase polynucleotide fragment #3017.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; 99.
XX
XX Homo sapiens.
OS
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX Disclosure; Page 252-254; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with the
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 3; Length 8222;
Best Local Similarity 99.2%; Pred. No. 4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGCAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010
Qy 61 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1011 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 1070
Qy 121 GT 122
Db 1071 CT 1072
RESULT 33
ABZ97144
ID ABZ97144 standard; DNA; 8222 BP.
XX
XX ABZ97144;
XX

```

DT 17-OCT-2003 (first entry)
XX Human nucleic acid sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytotatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 12386; 872pp; English.
PS
PS The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytotatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;
PS
PS
PS Query Match 46.7%; Score 120.4; DB 10; Length 8222;
PS Best Local Similarity 99.2%; Pred. No. 4e-24;
PS Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGACTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
DB 951 CAGCGGAGTGATGGCAAGCAGACTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 120
DB 1011 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 1070
QY 121 GT 122
DB 1071 CT 1072

RESULT 34
ABD19730
ID ABD19730 standard; DNA; 8222 BP.
XX
XX ABD19730;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human inducible nitric oxide synthase DNA fragment 1897.
DE
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; cytotatic; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
XX
XX WO200285309-A2.
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 12386; 763pp; English.
PS
PS This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating.
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytotatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 SQ Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 11; Length 8222;
 Best Local Similarity 99.2%; Pred. No. 4e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 951 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
 QY 61 GGCTACCAAGTCCAGATGCGAGCATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 120
 DB 1011 GGCTACCAAGTCCAGATGCGAGCATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 1070
 QY 121 GT 122
 DB 1071 CT 1072
 RESULT 35
 AAA34820
 ID AAA34820 standard; DNA; 9513 BP.
 AC AAA34820;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2509.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-2055971/18.
 XX
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 666-669; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;
 Query Match 46.7%; Score 120.4; DB 3; Length 9513;
 Best Local Similarity 99.2%; Pred. No. 4.1e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 2242 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 2301
 QY 61 GGCTACCAAGTCCAGATGCGAGCATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 120
 DB 2302 GGCTACCAAGTCCAGATGCGAGCATCAGAGGGGACCTGCCACAGTGGGAATTCACCTCAG 2361
 QY 121 GT 122
 DB 2362 CT 2363
 RESULT 36
 AAF20942
 ID AAF20942 standard; DNA; 9513 BP.
 XX
 AC AAF20942;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide #2509.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI (NYCE/) NYCE J W.
 XX
 DR Nyce JW;
 WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

XX Disclosure; Page 737-739; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
XX the present invention

SQ Sequence 9513 BP; 2107 A; 2868 C; 2672 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 3; Length 9513;
Best Local Similarity 99.2%; Pred. No. 4.1e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
DB 2242 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 2301

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
DB 2302 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 2361

QY 121 GT 122
DB 2362 CT 2363

RESULT 37
ID ABZ96636

XX ABZ96636 standard; DNA; 9513 BP.

XX AC ABZ96636;

XX 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory, antiallergic;
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

OS: Homo sapiens.

PN WO200295308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

DR Pharmacutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 11878; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antialasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 10; Length 9513;
Best Local Similarity 99.2%; Pred. No. 4.1e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
DB 2242 CAGCGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 2301

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
DB 2302 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 2361

QY 121 GT 122

DB 2362 CT 2363

RESULT 38
ABD20500

ID ABD20500 standard; DNA; 9513 BP.

XX AC ABD20500;

XX 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #111.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
XX WO200285309-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 11893; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 11; Length 9513;
Best Local Similarity 99.2%; Pred. No. 4.1e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 CAGCGGAGTGATGCGCAAGCAGACTTCGCGGTGGGAATGCTCAGCTCATCGCTATGCT 60
|||||

Db 2242 CAGCGGAGTGATGCGCAAGCAGCAGACTTCGCGGTGGGAATGCTCAGCTCATCGCTATGCT 2301
Qy 61 GGTACACAGATGCCAGATGCCAGATCAGAGGGGACCTCCCAACGTGGAAATTCACCTCAG 120
|||
Db 2302 GGTACACAGATGCCAGATGCCAGATCAGAGGGGACCTCCCAACGTGGAAATTCACCTCAG 2361
Qy 121 GT 122
Db 2362 CT 2363
RESULT 39
AAF21436
ID AAF21436 standard; DNA; 35384 BP.
XX
XX AAF21436;
DT 14-MAR-2001 (first entry)
XX
XX Human enzyme-related antisense polynucleotide #3003.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US008020.
XX
XX 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX Nyce JW;
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX Disclosure; Page 47-55; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders

CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 35384 BP; 7013 A; 10128 C; 10025 G; 7883 T; 0 U; 335 Other;

Query Match 46.7%; Score 120.4; DB 3; Length 35384;
Best Local Similarity 99.2%; Pred. No. 5.5e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60
DB 28113 CAGCGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 28172

QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 120
DB 28173 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 28232

QY 121 GT 122
DB 28233 CT 28234

RESULT 40
ABZ97130
ID ABZ97130 standard; DNA; 35459 BP.
AC ABZ97130;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 12372; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 35459 BP; 7025 A; 10160 C; 10041 G; 7897 T; 0 U; 336 Other;

Query Match 46.7%; Score 120.4; DB 10; Length 35459;
Best Local Similarity 99.2%; Pred. No. 5.5e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60
DB 28188 CAGCGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 28247

QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 120
DB 28248 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 28307

QY 121 GT 122
DB 28308 CT 28309

Search completed: December 13, 2005, 16:32:42
Job time : 476 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 15:55:10 ; Search time 3759 Seconds
(without alignments)
3211.244 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 cagcgagtgatggcaagca.....ttgtcccccagctgtgcatc 258

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_est8.*
10: gb_gse2.*
11: gb_gse3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.4	46.7	2994	11	DQ047444 Homo sapi
2	120.4	46.7	2994	11	DQ047445 Pan trogl
3	108.2	41.9	453	9	AQ214630 HS 3117 A
4	104.4	40.5	553	1	AW654110 103369 MA
5	98.2	38.1	523	9	AQ800595 HS 5314 B
6	93.6	36.3	518	9	AQ720606 HS 5542_B
7	90.2	35.0	842	9	CC520102 CH240_367
8	78.2	30.3	3437	10	AY419784 Homo sapi
9	77.2	29.9	486	10	CG668876 OST465233
10	77.2	29.9	526	10	CG506126 OST55467
11	77.2	29.9	3420	10	AY419786 Mus muscu
12	77.2	29.9	5622	4	BC083183 Mus muscu
13	77.2	29.9	5626	4	BC066101 Mus muscu
14	76.8	29.8	3430	10	AY419785 Pan trogl
15	74.6	28.9	540	10	CG650955 OST410927
16	74	28.7	820	6	CF251860 hdm005_c0
17	74	28.7	892	5	BU125423 603151629
18	72.8	28.2	581	11	AL125664 Fugu rubr
19	70	27.1	621	9	AZ231351 RPCI-23-8
20	69.8	27.1	581	11	AL125676 Fugu rubr
21	67.4	26.1	470	9	AQ095690 HS 3017 A
22	64.4	25.0	520	5	BQ551961 H4U12E1I-

23	64.4	25.0	711	3	BM950581	BM950581 UI-M-EH0P
24	64.4	25.0	843	7	CN527461	CN527461 UI-M-HQ0-
25	64.4	25.0	4120	4	AK077896	AK077896 Mus muscu
26	64	24.8	660	6	CF744130	CF744130 UI-M-GV0-
27	61.2	23.7	544	8	CX385385	CX385385 JGI_XZT65
28	61.2	23.7	721	3	BP178167	BP178167 BP178167
29	54.8	21.2	286	9	AZ044226	AZ044226 RPCI-23-3
30	54.8	21.2	3612	11	DQ045247	DQ045247 Homo sapi
31	49.4	19.1	625	3	BJ088070	BJ088070 BJ088070
32	48.6	18.8	619	11	FR0038157	AL125658 Fugu rubr
33	46.8	18.1	3449	11	DQ045248	DQ045248 Pan trogl
34	45.2	17.5	506	7	CK016997	CK016997 AGENCOURT
35	43.2	16.7	688	5	BU425320	BU425320 603961089
36	42.4	16.4	1171	8	DR123141	DR123141 49091370
37	40.2	15.6	567	8	DN757217	DN757217 GL-CF-140
38	39.8	15.4	797	1	AJ394075	AJ394075 AJ394075
39	39.6	15.3	771	7	CN459880	CN459880 UI-M-HB0-
40	39.4	15.3	721	3	BJ733387	BJ733387 BJ733387
41	39.2	15.2	925	10	CNS0091P	AL053013 Drosophila
42	38.8	15.0	657	6	CA090625	CA090625 SCSGAN210
43	38.8	15.0	692	7	CO570671	CO570671 AGENCOURT
44	38.6	15.0	301	4	AK185276	AK185276 Mus muscu
45	38.6	15.0	311	5	BX919466	BX919466 BX919466

ALIGNMENTS

RESULT 1	DQ047444	2994 bp	DNA	linear	GSS 02-JUN-2005
LOCUS	Homo sapiens NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	genomic survey sequence.				
ACCESSION	DQ047444				
VERSION	DQ047444.1	GI:66900643			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees				
JOURNAL	(er) PLOS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 2994)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
FEATURES	Location/Qualifiers				
source	1. .2994				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/chromosome="17"				
	<1. .2994				
	/gene="NOS2A"				
	/locus_tag="HC15370"				
gene					
ORIGIN					
Query Match	46.7%	Score 120.4;	DB 11;	Length 2994;	
Best Local Similarity	99.2%	Pred. No. 6.7e-21;			
Matches	121;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;

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QY      1  CAGCGGAGTGATGGCAACGACGACTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      745 CAGCGGAGTGATGGCAACGACGACTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 804

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db      805  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 864

QY      121  GT 122
Db      865  CT 866

RESULT 2
DQ047445
LOCUS      2994 bp      DNA      linear      GSS 02-JUN-2005
DEFINITION Pan troglodytes NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION  DQ047445
VERSION    DQ047445.1 GI:66900644
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
REFERENCE  1 (bases 1 to 2994)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
             Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
             White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
             Chimpanzees
JOURNAL   (et) PLOS Biol. 3 (6), E170 (2005)
PUBMED    15869325
REFERENCE  2 (bases 1 to 2994)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
             Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
             White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment. Translation starts at the beginning of
             alignment.
FEATURES   Location/Qualifiers
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               1..2994
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               /mol_type="genomic DNA"
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               /locus_tag="HC15370"

ORIGIN
Query Match      46.7%; Score 120.4; DB 11; Length 2994;
Best Local Similarity 99.2%; Pred. No. 6.7e-21;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAACGACGACTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      745 CAGCGGAGTGATGGCAACGACGACTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 804

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db      805  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 864

QY      121  GT 122
Db      865  CT 866

RESULT 3

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AQ214630/c
LOCUS      453 bp      DNA      linear      GSS 18-SEP-1998
DEFINITION HS_3117_A1_F08_T7 CIT Approved Human Genomic Sperm Library D Homo
             sapiens genomic clone Plate=3117 Col=15 Row=K, genomic survey
             sequence.
ACCESSION  AQ214630
VERSION    AQ214630.1 GI:3625831
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 453)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
             Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
             Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
             scanning the human genome
JOURNAL   Proc Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED    1049764
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
             High Throughput Sequencing Center
             University of Washington
             401 Queen Anne Avenue North, Seattle, WA 98109, USA
             Tel: (206) 616-3618
             Fax: (206) 616-3887
             Email: jwallace@u.washington.edu
             Sequence Tagged Connector
             Plate: 3117 row: K column: 15
             Class: BAC ends
             High quality sequence stop: 453.
FEATURES   Location/Qualifiers
             source
               1..453
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /Clones="Plate=3117 Col=15 Row=K"
               /sex="male"
               /clone_lib="CIT Approved Human Genomic Sperm Library D"
               /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
               E-Coli DH10B"

ORIGIN
Query Match      41.9%; Score 108.2; DB 9; Length 453;
Best Local Similarity 94.0%; Pred. No. 8.2e-16;
Matches 110; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      140 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGCTGTGGATGCTCAGCTCATCCGCTATGCT 81

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCT 117
Db      80  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCT 24

RESULT 4
AW654110
LOCUS      553 bp      mRNA      linear      EST 25-APR-2001
DEFINITION 103369 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  AW654110
VERSION    AW654110.1 GI:7419936
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
             Pecora; Bovidae; Bovinae; Bos.
AUTHORS   1 (bases 1 to 553)
             Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
             Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
             Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,

```

Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 11282978

CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 95 row: L column: 4

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1. .553

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 1BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."

FEATURES

source

ORIGIN

Query Match 40.5%; Score 104.4; DB 1; Length 553;

Best Local Similarity 91.0%; Pred. No. 8.5e-17;

Matches 111; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 69 CAGCGAGCGATGGGAGCATGACTTCGGGTCTGGAAACGCCAGCTCATCCGCTATGCC 128

Qy 61 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAAGTGGAAATTCACATCAG 120

Db 129 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAAGTGGAGTTACACAG 188

Qy 121 GT 122

Db 189 CT 190

RESULT 5

AQ800595/c

LOCUS

DEFINITION HS_5314_B2 D01 T7A RPCI-11 Human Male BAC Library Homo sapiens

genomic clone Plate=890 Col=2 Row=H, genomic survey sequence.

ACCESSION AQ800595

VERSION AQ800595.1 GI:5717850

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 523)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 Plate: 890 row: H column: 2
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 523.

FEATURES

source

Location/Qualifiers

1. .523

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="Plate=890 Col=2 Row=H"

/sex="male"

/clone_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"

ORIGIN

Query Match 38.1%; Score 98.2; DB 9; Length 523;

Best Local Similarity 96.2%; Pred. No. 3.6e-15;

Matches 100; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 139 CAGCGAGTGATGCGACGACGACTTCGGGTGGAATGCTCAGATCCGCTATGCT 80

Qy 61 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCAA 104

Db 79 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCTGCCCTA 36

RESULT 6

AQ720606/c

LOCUS

DEFINITION HS_5542_B1_H02_T7A RPCI-11 Human Male BAC Library Homo sapiens

genomic clone Plate=1118 Col=3 Row=P, genomic survey sequence.

ACCESSION AQ720606

VERSION AQ720606.1 GI:5480275

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 518)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 1118 row: P column: 3

Seq primer: T7

Class: BAC ends

High quality sequence stop: 518.

Location/Qualifiers

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/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

FEATURES
source

Query Match 36.3%; Score 93.6; DB 9; Length 518;
Best Local Similarity 95.0%; Pred. No. 5.8e-14;
Matches 96; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ORIGIN

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Query Match      35.0%; Score 90.2; DB 9; Length 842;
Best Local Similarity 76.9%; Pred. No. 4.9e-13;
Matches 110; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      471 CAGAGGACCGACGACGACGAGCTTCGGCTTTGGAACTCCCACTCATCCGCTACGCT 530

Qy      61 GGCTACAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTAG 120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      531 GGCTACAGCAGCCGACGCGGCTCCATCCTGGGGAGCCAGCAACGTGGAGTTCACGGAG 590

Qy      121 GTACCGCGCCGAGCCTCAGCCRC 143
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Db      591 GTAGCGCGCCCGCCGCTCCCTCC 613
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RESULT 7
CC520102
LOCUS
DEFINITION
CH240_367118.T7 CHORI-240 Bos taurus genomic clone CH240_367118,
genomic survey sequence.

ACCESSION
CC520102
VERSION
CC520102.1 GI:31838390
KEYWORDS
GSS.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P. and Fellam, R.

TITLE
JOURNAL
COMMENT
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_367118.TARBAC13P2

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rholt@bccsc.ca

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering.information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 367 row: I column: 18

Seq primer: T7

Class: BAC ends.

FEATURES
source

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_367118"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"

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/note="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull Li Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 35.0%; Score 90.2; DB 9; Length 842;
Best Local Similarity 76.9%; Pred. No. 4.9e-13;
Matches 110; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Db 471 CAGAGGACCGACGACGACGAGCTTCGGCTTTGGAACTCCCACTCATCCGCTACGCT 530

Qy 61 GGCTACAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTAG 120
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 531 GGCTACAGCAGCCGACGCGGCTCCATCCTGGGGAGCCAGCAACGTGGAGTTCACGGAG 590

Qy 121 GTACCGCGCCGAGCCTCAGCCRC 143
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Db 591 GTAGCGCGCCCGCCGCTCCCTCC 613

RESULT 8
AY419784
LOCUS
DEFINITION
AY419784
Homo sapiens NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY419784
VERSION
AY419784.1 GI:39775741
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE
JOURNAL
COMMENT
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)

REFERENCE
PUBMED
14671302
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source

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1..3437
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/ gene="NOS1"
/ locus_tag="HCW7006"

ORIGIN

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Best Local Similarity 77.2%; Pred. No. 8.7e-10;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGACGACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Db 553 CAGAGACAGAGCGCAGACGACTTCGAGTCTGGAATCCGAGCTCATCCGCTACGCT 612
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QY 61 GGTCTACCATGCGCATGCGCAGATCAGAGGGAGCCCTGCCAACTGGAATTCATCTCAG 120
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Db 613 GGTCTACAGCAGCTGACGGCTCCACCCTGGGGAGCCAGCCCAATGTGCAGTTCACAGAG 672

QY 121 GTA 123
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Db 673 ATA 675

RESULT 9
CG568876      486 bp      mRNA      linear      GSS 02-OCT-2003
LOCUS      OST465233 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST465233,
DEFINITION      mRNA sequence.
ACCESSION      CG568876
VERSION
KEYWORDS
SOURCE      GSS.
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 486)
AUTHORS      Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
PUBMED
COMMENT      Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="OST465233"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

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Best Local Similarity 77.0%; Pred. No. 1.2e-09;
Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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ORIGIN

Query Match      30.3%; Score 78.2; DB 10; Length 3437;
Best Local Similarity 77.2%; Pred. No. 8.7e-10;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGACGACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
   |||||
Db 553 CAGAGACAGAGCGCAGACGACTTCGAGTCTGGAATCCGAGCTCATCCGCTACGCT 612
   |||||

QY 61 GGTCTACCATGCGCATGCGCAGATCAGAGGGAGCCCTGCCAACTGGAATTCATCTCAG 120
   |||||
Db 613 GGTCTACAGCAGCTGACGGCTCCACCCTGGGGAGCCAGCCCAATGTGCAGTTCACAGAG 672

QY 121 GTA 122
   ||
Db 124 AT 125

RESULT 10
CG506126      526 bp      mRNA      linear      GSS 01-OCT-2003
LOCUS      OST55467 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST55467,
DEFINITION      mRNA sequence.
ACCESSION      CG506126
VERSION      CG506126.1 GI:37284915
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 526)
AUTHORS      Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
PUBMED
COMMENT      Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
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/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

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Best Local Similarity 77.0%; Pred. No. 1.2e-09;
Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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QY 61 GGTCTACCATGCGCATGCGCAGATCAGAGGGAGCCCTGCCAACTGGAATTCATCTCAG 120
   |||||
Db 77 GGTCTACAGCAGCCAGATGGCTCTACCTTGGGCGATCCAGCTAATGTGCAGTTCACAGAG 136
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QY 121 GT 122
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Db 137 AT 138

RESULT 11
AY419786

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LOCUS	AY419786	3420 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Mus musculus NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY419786				
VERSION	AY419786.1	GI:39775743			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
	1 (bases 1 to 3420)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 3420)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence as made by sequencing genomic exons and ordering them based on alignment.				
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Best Local Similarity	77.0%; Pred. No. 1.6e-09;				
Matches	94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;				
QY	1 CAGCGAGTGATGCGAAGCAGCATCTCCGGTGTGGAACTGCTCAGCTCATCCGCTATGCT 60				
Db	553 CAAAGGAGTGTATGGCAAGCATGACTTCGAGTGTGGAACTCGCAGCTCATCCGCTATGCC 612				
QY	61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACATCAG 120				
Db	613 GGCTACAGCAGCCAGATGGCTCTACCTTGGCGATCCAGTATGTGGAGTTCACAGAG 672				
QY	121 GT 122				
Db	673 AT 674				
RESULT 12					
LOCUS	BC083183	5622 bp	mRNA	linear	HTC 30-MAR-2005
DEFINITION	Mus musculus nitric oxide synthase 1, neuronal, mRNA (cDNA clone IMAGE:30533636), containing frame-shift errors.				
ACCESSION	BC083183				
VERSION	BC083183.1	GI:52789385			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
	1 (bases 1 to 5622)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villallon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
Mammalian Gene Collection Program Team	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903 (2002)				
12477932	2 (bases 1 to 5622)				
NIH MGC Project	Direct Submission				
Submitted (24-SEP-2004)	National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA				
NIH-MGC Project URL:	http://mgc.nci.nih.gov				
Contact:	MGC help desk				
Email:	cgapbs-rc@mail.nih.gov				
Tissue Procurement:	Dr. James Lin, University of Iowa				
cDNA Library Preparation:	M. Bento Soares, University of Iowa				
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by:	National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;				
Web site:	http://www.nisc.nih.gov/				
Contact:	nisc_mgc@hgrl.nih.gov				
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maekeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.					
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
Series:	IRAK Plate: 176 Row: 0 Column: 2				
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320	This clone has the following problem: frame shifted.				
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	/lab_host="DH10B"				
	/note="Vector: pYX-ASC"				
ORIGIN					
Query Match	29.9%; Score 77.2; DB 4; Length 5622;				
Best Local Similarity	77.0%; Pred. No. 1.7e-09;				
Matches	94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;				
QY	1 CAGCGGAGTGATGCGAAGCAGCATCTCCGGTGTGGAACTGCTCAGCTCATCCGCTATGCT 60				
Db	1860 CAAAGGACTGATGCGAAGCATGACTTCGAGTGTGGAACTCGCAGCTCATCCGCTATGCC 1919				

QY 61 GGCTACAGATCCAGATCGAGCATCAGAGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
 Db 1920 GGCTACAGAGCCAGATGGCTCTACCTTGGGGGATCCAGCTATAGTGGAGTTCACAGAG 1979

QY 121 GT 122
 Db 1980 AT 1981

RESULT 13
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 LOCUS
 DEFINITION Mus musculus nitric oxide synthase 1, neuronal, mRNA (cDNA clone IMAGE:30533636), containing frame-shift errors.
 ACCESSION BC066101
 VERSION BC066101.1 GI:41946848
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 5626)
 Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ussin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

2 (bases 1 to 5626)
 Strausberg, R.

Direct Submission
 Submitted (02-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.uiowa.edu>

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu

Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fiehler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>

Series: Plate: Row: Column: 0

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320

This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:10090"
 /clone="IMAGE:30533636"
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 /note="Vector: pYX-ASC"

ORIGIN

Query Match 29.9%; Score 77.2; DB 4; Length 5626;
 Best Local Similarity 77.0%; Pred. No. 1.7e-09;
 Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAGCAGCTTCGGGTGTGGATGCTCAGCTATCGCTATGCT 60

Db 1860 CAAGGAGCTGTGGCAGCATGACTTCGAGTGTGGAACTCGCAGCTATCGCTATGCC 1919

QY 61 GGCTACCATCCAGATCCAGATGGCAGCATCAGAGGGACCCCTGCCAACGTGGAATTCACCTCAG 120

Db 1920 GGCTACAGCAGCAGATGGCTCTACCTTGGCGATCCAGCTAATGTGGAGTTCACAGAG 1979

QY 121 GT 122

Db 1980 AT 1981

RESULT 14

AV419785

LOCUS Pan troglodytes NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY419785

VERSION AY419785.1 GI:39775742

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 3430)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBLISHED 14671302

REFERENCE 2 (bases 1 to 3430)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

JOURNAL COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

1..3430

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1_>3430

/gene="NOS1"

/locus_tag="HCM7006"

ORIGIN

Query Match 29.8%; Score 76.8; DB 10; Length 3430;
 Best Local Similarity 77.5%; Pred. No. 2e-09; 27; Indels 0; Gaps 0;
 Matches 93; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 |||||
 Db 546 CAGAGCAGACGGCGAAGCAGACTTCGGAGTCTGGAATCCAGCTCATCCGCTACGCT 605
 |||||
 QY 61 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCTGCCAAGCTGGAAATTCACCTCAG 120
 |||||
 Db 606 GGCTACAAGCAGCCCGACGGCTCCACCTGGGGGACCCAGCCCAATGTGCAGTTCACAGAG 665
 |||||

RESULT 15

CG650955 540 bp mRNA linear GSS 02-OCT-2003
 LOCUS OST410927 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST410927,
 mRNA sequence.

ACCESSION CG650955

VERSION CG650955.1 GI:37474804

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 540)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Figgott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
 Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL

PUBMED

COMMENT

14510273 Contact: Zambrowicz BP

OmiBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

FEATURES

source

Location/Qualifiers
 1..540
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST410927"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 28.9%; Score 74.6; DB 10; Length 540;
 Best Local Similarity 75.4%; Pred. No. 5.8e-09;
 Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 |||||
 Db 27 CAAAGACTGTATGGCAAGCATGACTTCGGAGTGTGGAATCGTCACTCATCCGCTATGCC 86
 |||||
 QY 61 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCTGCCAAGCTGGAAATTCACCTCAG 120
 |||||
 Db 87 GGCTACAAGCAGCCCGACGGCTCTACCTTGGCGATCCAGCTAATGTGGAGTTCACAGAG 146
 |||||

121 GT 122

147 AT 148

RESULT 16

LOCUS

DEFINITION

CF251860 820 bp mRNA linear EST 07-AUG-2003
 hdm005_c06 LPS-activated macrophage cell line Gallus gallus cDNA,
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF251860.1 GI:33485115
 EST.
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 820)
 Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J.,
 Chausse,A.M. and Zoorob,R.
 A collection of chicken ESTs from activated immune cells
 Unpublished (2003)
 Contact: Zoorob R
 UPR 1983

CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France

Tel: 33 1 49 58 35 00

Fax: 33 1 49 58 33 81

Email: zoorob@vjf.cnrs.fr.

Location/Qualifiers

1..820

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/cell_line="HD11"

/clone_lib="LPS-activated macrophage cell line"

/notes="Vector: pTriplEx2"

ORIGIN

Query Match 28.7%; Score 74; DB 6; Length 820;
 Best Local Similarity 75.4%; Pred. No. 9e-09;
 Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10
11. Feature 11	Source 11
12. Feature 12	Source 12
13. Feature 13	Source 13
14. Feature 14	Source 14
15. Feature 15	Source 15
16. Feature 16	Source 16
17. Feature 17	Source 17
18. Feature 18	Source 18
19. Feature 19	Source 19
20. Feature 20	Source 20
21. Feature 21	Source 21
22. Feature 22	Source 22
23. Feature 23	Source 23
24. Feature 24	Source 24
25. Feature 25	Source 25
26. Feature 26	Source 26
27. Feature 27	Source 27
28. Feature 28	Source 28
29. Feature 29	Source 29
30. Feature 30	Source 30
31. Feature 31	Source 31
32. Feature 32	Source 32
33. Feature 33	Source 33
34. Feature 34	Source 34
35. Feature 35	Source 35
36. Feature 36	Source 36
37. Feature 37	Source 37
38. Feature 38	Source 38
39. Feature 39	Source 39
40. Feature 40	Source 40
41. Feature 41	Source 41
42. Feature 42	Source 42
43. Feature 43	Source 43
44. Feature 44	Source 44
45. Feature 45	Source 45
46. Feature 46	Source 46
47. Feature 47	Source 47
48. Feature 48	Source 48
49. Feature 49	Source 49
50. Feature 50	Source 50
51. Feature 51	Source 51
52. Feature 52	Source 52
53. Feature 53	Source 53
54. Feature 54	Source 54
55. Feature 55	Source 55
56. Feature 56	Source 56
57. Feature 57	Source 57
58. Feature 58	Source 58
59. Feature 59	Source 59
60. Feature 60	Source 60
61. Feature 61	Source 61
62. Feature 62	Source 62
63. Feature 63	Source 63
64. Feature 64	Source 64
65. Feature 65	Source 65
66. Feature 66	Source 66
67. Feature 67	Source 67
68. Feature 68	Source 68
69. Feature 69	Source 69
70. Feature 70	Source 70
71. Feature 71	Source 71
72. Feature 72	Source 72
73. Feature 73	Source 73
74. Feature 74	Source 74
75. Feature 75	Source 75
76. Feature 76	Source 76
77. Feature 77	Source 77
78. Feature 78	Source 78
79. Feature 79	Source 79
80. Feature 80	Source 80
81. Feature 81	Source 81
82. Feature 82	Source 82
83. Feature 83	Source 83
84. Feature 84	Source 84
85. Feature 85	Source 85
86. Feature 86	Source 86
87. Feature 87	Source 87
88. Feature 88	Source 88
89. Feature 89	Source 89
90. Feature 90	Source 90
91. Feature 91	Source 91
92. Feature 92	Source 92
93. Feature 93	Source 93
94. Feature 94	Source 94
95. Feature 95	Source 95
96. Feature 96	Source 96
97. Feature 97	Source 97
98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

	Query Match	27.1%	Score 59.8	DB 11	Length 581	
	Best Local Similarity	71.8%	Pred. No. 1.1e-07			
	Matches 89	Conservative 0	Mismatches 35	Indels 0	Gaps 0	
Qy	1	CAGGGAGTCATGSCAAGCAGCACTCCGGGTGTGGAACTGCTAGCTCATCCGGTATGCT	60			
Db	380	CCGAGGACAGATGSCAAACATGACTTTTCGAGGTGTGGAAACAGCTAGCTGATTCGGTATGCT	321			
Qy	61	GGGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCGTCCACACGTGGAATTCACCTCAG	120			

Qy	121	GTAC	124
Db	260	GTGC	257

RESULT 21
 AQQ95690/c
 LOCUS
 AQQ95690 470 bp DNA linear GSS 27-AUG-1998
 DEFINITION
 HS_3017_Al_F08_MR CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3017 Col=15 Row=A, genomic survey
 sequence.

RESULT 21
 AQQ95690/c
 LOCUS
 AQQ95690 470 bp DNA linear GSS 27-AUG-1998
 DEFINITION
 HS_3017_Al_F08_MR CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3017 Col=15 Row=A, genomic survey
 sequence.

RESULT 21
 AQQ95690/c
 LOCUS
 AQQ95690 470 bp DNA linear GSS 27-AUG-1998
 DEFINITION
 HS_3017_Al_F08_MR CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3017 Col=15 Row=A, genomic survey
 sequence.

ORIGIN		E-COLL DRIVES	
Query Match	26.1%;	Score 67.4;	DB 9;
Best Local Similarity	98.8%;	Prod No 4.5e-07;	Length 470;
Matches	68;	Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	1	CAGCGAGTGATGGCAGACGACTCCGGGTGGAA	TGCTCAGCTCATCCGGTATGCT 60

```

Db      69  CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 10
QY      61  GGCTACGAG 69
        |||||
Db      9  GGCTACGAG 1

RESULT 22
LOCUS   BQ551961
DEFINITION H4012E11-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
ACCESSION BQ551961
VERSION   BQ551961.1
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 520)
AUTHORS   VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
          Martin,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamatani,T.,
          Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and KO,M.S.H.
TITLE     Assembly, verification, and initial annotation of NIA 7.4K mouse
          cDNA clone set
JOURNAL   Genome Res. 12 (12), 1999-2003 (2002)
PUBMED    12466305
COMMENT   Other ESTs: H4012E11-3
          Contact: Yong Qian
          Laboratory of Genetics
          National Institute on Aging/National Institutes of Health
          333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
          Email: cdna@lgaun.grc.nia.nih.gov
          This clone set has been freely distributed to the community. Please
          visit http://lgaun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
          Plate: H4012 row: E column: 11
          Seq primer: -21M13 Reverse
          High quality sequence stop: 520
          POLYA=No.

FEATURES             Location/Qualifiers
     source            1..520
     mol_type="mRNA"   /organism="Mus musculus"
     strain="C57BL/6"   /mol_type="mRNA"
     db_xref="niaEST:H4012E11-5"
     /db_xref="taxon:10090"
     /clones="H4012E11"
     /sex="mixed"
     /dev_stage="mixed"
     /lab_host="DH10B"
     /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
     /note="vector: pSPORT1; Site.1: SalI; Site.2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN
Query Match      25.0%; Score 64.4; DB 5; Length 520;
Best Local Similarity 70.5%; Pred. No. 2.8e-06;
Matches 86; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 60
Db      8  CAGCGGTGCTTCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 67
QY      61  GGCTACGAGTGCCAGATGGCAGATGGCTCCGTCGAGGGGACCTGCCACGCTGGGAATTCACCTCAG 120
Db      68  GGCTATAGGACGACGAGATGGCTCCGTCGAGGGGACCTGCCACGCTGGGAATTCACCTCAG 127
QY      121  GT 122
Db      128  CT 129

RESULT 23
LOCUS   BM950581
DEFINITION UI-M-EH0p-buu-d-15-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
ACCESSION BM950581
VERSION   BM950581.1
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 711)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Dr. James Lin, University of Iowa
          cDNA library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          This clone was contributed by the Brain Molecular Anatomy Project
          (BMAP)
          Seq primer: pYX-5.

FEATURES             Location/Qualifiers
     source            1..711
     mol_type="mRNA"   /organism="Mus musculus"
     strain="C57BL/6"   /mol_type="mRNA"
     db_xref="taxon:10090"
     /clone="IMAGE:5687006"
     /tissue_type="whole brain"
     /dev_stage="embryo 18.5 dpc"
     /lab_host="DH10B (T1 phage resistant)"
     /clone_lib="NIH_BMAP_EH0p"
     /note="Organ: Brain; Vector: pYX-Asc; Site.1: EcoR I;
          Site.2: Not I; The library was constructed according to
          Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
          1996. Denatured mRNA was size fractionated on a 1% agarose
          gel. First strand cDNA synthesis was primed with an
          oligo-dT primer containing a Not I site. Double stranded
          cDNA was size selected according to mRNA size fraction,
          ligated with EcoR I adaptor, digested with Not I, and then
          cloned directionally into pYX-Asc vector. The library tag
          sequence located between the Not I site and the polyA
          tail, is CAGCCAGGAC. This library was created for the
          University of Iowa Mouse Brain Molecular Anatomy Project
          (BMAP). 'Gene Discovery in the Developing Mouse Nervous
          System', supported by National Institute of Mental Health
          (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match      25.0%; Score 64.4; DB 3; Length 711;
Best Local Similarity 70.5%; Pred. No. 2.9e-06;
Matches 86; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 60
Db      32  CAGCGGTGCTTCGGGTGTGGAATGCTCAGCTCATCCGATATGCT 91
QY      61  GGCTACGAGTGCCAGATGGCAGATGGCTCCGTCGAGGGGACCTGCCACGCTGGGAATTCACCTCAG 120
Db      92  GGCTATAGGACGACGAGATGGCTCCGTCGAGGGGACCTGCCACGCTGGGAATTCACCTCAG 151
QY      121  GT 122
Db      152  CT 153

```


Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES

source
1..4120
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:6030422B05"
/clone="6030422B05"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
22..3630
/notes="unnamed protein product; nitric oxide synthase 3,
endothelial cell (MGI:97362, GB|NM_008713, evidence:
BLASTN, 9%, match=3633)
putative"
/codon_start=1
/protein_id="BAC37052.1"
/db_xref="GI:26346807"
/translation="MGNLSVSGQEPGPGGLGLGLGKGGPASPAPPSQAPAP
PSPTRPAPHSPLTPPDGPRFRVNWVEVGSITDYLTAQAQGGPCTSRCLGSL
VPPKQLSRPTQSPTEQLLQARDFIQWYNSIRSGSQAEHQEVEAEVAATG
TYQLRESLFTGAKARNAPRCVRIQWGLQVDFARDCTAQEFTYCNHIAAT
NGLTAFVIFVPCPGDGRFIRWNSQLIRYAGYQDGSVRGDFANVEITELCIQH
GWTPEGNRFVLLQAPDEPPELFTLPEMVLVPLEHPTLEWAAELGLRWYALPA
VSNMLIEGLEPFPAPPSWYNSSEIGWDLCDPHRYNILEDAVCMDLDTPTTSSL
WKAADAEINVAIHSIQLAKVTIVDHAATATSMKLENEQKRGCCADANWIVPP
ISGSLTPVPHQWVNTYSPAFRYPQDPWKGSAAGATIRKTKFEVAVNKKVSASL
MGTVMKRVKATILYSEAGRAQSYAQLGLFRKAPDPRVLCMDYDVVLSLEALV
LVTSTFGNDPPENGESFAAALMEMSGPYNSPRPEOHKSYKIRFNSVSCDPLVSS
WRKRKESNTDSAGALGTLCFCVGLGSRAPYHFCAPAFADVTRLEELGRLQLG
QGBELCQGEAFRGAQAQAAACETFCVGEDAKAARDIFSFKRQKQVRLSTQA
ESQLLPLGLTHVRRKMFQATILSVENLQSKSTRATILVRLDTGQSGEQYQPGDHI
GVCPPNRPGLVEALLSRVEDPPSPTEVAVEQKSGPGPPGPPGWRDRLPCTLRQ
ALTYFLDITSPSPRLIRLLSLTAESSEQLEALSQDPRPEWKEWKFSCPTLLLEVL
EQPSVALPAGLITLQPLQPRYSVSSAPSPGHEIHLTIATVATDQGLPLHY
GVCSWMSQLKADGPPCFIRGAPSPRLPDNPLCPLVCGPGTGIAPFGFMDRLHD
IEINGQPAPMTLVFGCRSQDLHVRDEVLDAQQGVFQCVLTATSRDPGSPKTYVQ
DLRLTEAAEVRHVLCEQGHMFVCGDVTWATSVLQTVQRILATEGMEGLDEAGDVIG
VLRDQQRHYEDIIFGLTLRTQEVTSRINTQSFSIQRQLRGAVPWSFDPGPPETPGS"

CDS

KEYWORDS

SOURCE
ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 660)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs@remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..660

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30620991"

/tissue_type="whole brain"

/dev_stage="1, 5, and 15 days newborn"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP GVO"

/note="Organ: Brain; Vector: pYX- Asc; Site 1: Ecor I;

Site 2: Not 1; The library was constructed according

Bonafide, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated with

Ecor I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is CGAATCTGAAT. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Query Match 24.8%; Score 64; DB 6; Length 660;

Best Local Similarity 76.0%; Pred. No. 3.7e-06;

Mismatches 0; Conservative 0; Gaps 0;

Matches 79; Indels 25;

Qy 19 CAGGAGTTCGGGTGGGAATGCTCAGCTCATCGCTATGCTGGCTACAGATGCCAGAT 78

Db 1 CATGACTTCGAGTGGGAACCTCGAGCTCATCGCTATGCTGGCTACAGATGCCAGAT 60

Qy 79 GCAGCATCAGAGGGGACCTGCCAACGTGGATTTCACCTCAGGT 122

Db 61 GGCTCTACCTTGGGGGATCCAGCTAATGTGGAGTTTCACAGAT 104

RESULT 27

CX385985

LOCUS

DEFINITION

IMAGE:7639850 5', mRNA sequence.

ACCESSION

CX385985.1

VERSION

EST.

KEYWORDS

Xenopus tropicalis (western clawed frog)

SOURCE

Xenopus tropicalis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match 25.0%; Score 64.4; DB 4; Length 4120;

Best Local Similarity 70.5%; Pred. No. 3.8e-06;

Mismatches 0; Conservative 0; Gaps 0;

Matches 86; Indels 36;

Qy 1 CAGCGGAGTGTGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

Db 715 CAGCGCTGCCCTGCGCGGGAGACTTCGGATCTGGAACAGCCAGCTGATACGCTATGCG 774

Qy 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTAG 120

Db 775 GCCTATAGCAGCAGGATGGCTCGCTGCGAGGGGACCCCGCCACCTGAGATCACTGAG 834

Qy 121 GT 122

Db 835 CT 836

RESULT 26

CF744130

LOCUS

DEFINITION

UI-M-GVO-clb-g-16-0-UI_r1 NIH BMAP_GVO Mus musculus cDNA clone

IMAGE:30620991 5', mRNA sequence.

ACCESSION

CF744130

VERSION

CF744130.1

GI:37640469

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 544)

AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.

TITLE DOE Joint Genome Institute Xenopus tropicalis EST project

JOURNAL Unpublished (2004)

COMMENT Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
<http://image.llnl.gov>

Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Small Insert: Based upon one or more sequencing reads of this clone where vector sequence was present at both ends, this clone has been determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: XZT 0677 row: 1 column: 24
High quality sequence stop: 544.

FEATURES

source 1, 544
Location/Qualifiers
1, 544
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7639850"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st, 36-41)"
/lab_host="E. coli XLI-Blue derivative, Stratagene Electropen-Blue"
/clone_lib="NIH XCC tropTrads"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108
(<http://mcb.berkeley.edu/labs/harland/pages/plasmids.html>)
."

ORIGIN

Query Match 23.7%; Score 61.2; DB 8; Length 544;
Best Local Similarity 68.9%; Pred. No. 2e-05;
Matches 84; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGTGGCAAGCAGCTCCGGGTGGAGTGTCTCAGCTCATCCGCTATGCT 60
|||||
Db 300 CAAGAACGGATGGGAAGCGTGACTTTAGATCTGGAATGCTCAGCTATTTCGCTATGCA 359
|||||

Qy 61 GCCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAAGTGGAAATTCACCTCAG 120
|||||
Db 360 GGATACAACAGCCTGATGGCTCAGTGTCTGGAGACCTGCAATGTAGATTGCACAGAG 419
|||||

Qy 121 GT 122
|
Db 420 AT 421

RESULT 28
BP178167
LOCUS BP178167 721 bp mRNA linear EST 10-OCT-2003
DEFINITION BP178167 mav3 Bombyx mori cdna clone mav30763, mRNA sequence.
ACCESSION BP178167
VERSION BP178167.1 GI:37648895

KEYWORDS

SOURCE Bombyx mori (domestic silkworm)

ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

REFERENCE

1 (bases 1 to 721)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cdna
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: knita@nias.affrc.go.jp

method:uni-directional, sequence direction:sequenced from T3 primer (5' -> 3').

FEATURES

source 1, 721
Location/Qualifiers
1, 721
/organism="Bombyx mori"
/mol_type="mRNA"
/strain="p50"
/db_xref="taxon:7091"
/clone="mav30763"
/tissue_type="Malpighian tubule"
/dev_stage="5th instar larva day 3"
/clone_lib="mav3"

ORIGIN

Query Match 23.7%; Score 61.2; DB 3; Length 721;
Best Local Similarity 68.9%; Pred. No. 2e-05;
Matches 84; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGTGGCAAGCAGCTCCGGGTGGAGTGTCTCAGCTCATCCGCTATGCT 60
|||||
Db 279 CAAGCACCAGCGGTAAACATGACTACAGATATGGAATCGGCAGCTTCAATTATGCA 338
|||||

Qy 61 GCCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAAGTGGAAATTCACCTCAG 120
|||||
Db 339 GGATACCAGGAGCCAGATGGAAGCATTATAGGAGATCCAGCAGAGTTGAATTTACAGAG 398
|||||

Qy 121 GT 122
|
Db 399 AT 400

RESULT 29

AZ044226
LOCUS RPCI-23-368A5.TV RPCI-23 Mus musculus genomic clone RPCI-23-368A5,
DEFINITION genomic survey sequence.

ACCESSION AZ044226

VERSION AZ044226.1 GI:7138883

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 286)

Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., McGann,S., Tsengaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSs: RPCI-23-368A5.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
 Plate: 368 row: A column: 5
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1. .286
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-368A5"
 /sex="Female"
 /lab_host="DH10B"
 /clone_lib="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 21.2%; Score 54.8; DB 9; Length 286;
 Best Local Similarity 75.2%; Pred. No. 0.0006;
 Matches 79; Conservative 1; Mismatches 24; Indels 1; Gaps 1;
 QY 60 TGGCTACAGATGCAGATCGACATCAGAGGGACCTGCCAACGTGAATCTACTCA 119
 Db 1 TGGCTACCANATGCCGATCGACATCAGAGGGAGTGTGCCACCTTGGAGTTCACCCA 60
 QY 120 GGTACCGCGCCAGCTCAGCCGCCATTTGGGGGGGAGCC 164
 Db 61 GGTA-CTGACTCAGCTCTCTAGATCCCTGTGTGGCGAGGGAGCC 104

RESULT 30
 DQ045247
 LOCUS Homo sapiens NOS3 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION DQ045247
 VERSION DQ045247.1 GI:66896462
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 3612)
 Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
 Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civeello,D.,
 White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 A Scan for Positively Selected Genes in the Genomes of Humans and
 Chimpanzees
 (er) PLOS Biol. 3 (6), E170 (2005)
 15869325
 2 (bases 1 to 3612)
 Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
 Hubisz,M.J., Fladel-Alon,A., Tanenbaum,D.M., Civeello,D.,
 White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment. Translation starts at the beginning of

alignment.
FEATURES
 Location/Qualifiers
 1. .3612
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="7"
 <1. .>3612
 /gene="NOS3"
 /locus_tag="HC11004"

ORIGIN

Query Match 21.2%; Score 54.8; DB 11; Length 3612;
 Best Local Similarity 65.6%; Pred. No. 0.0013;
 Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGAATGCTCAGCTATCGCTATGCT 60
 Db 697 CAGCGCTGCCCTGGCGGAGGAGACTTCCGAATCTGAACAGCAGCTGTGGCTACGGC 756
 QY 61 GGTACACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
 Db 757 GGTACCGCAGCAGCAGCGCTCTGTGCGGGGGACCCAGCCACGTGGAGATCACCGAG 816
 QY 121 GT 122
 Db 817 CT 818

RESULT 31

BJ088070
 LOCUS BJ088070 NIBB Mochii normalized Xenopus tailbud library Xenopus
 DEFINITION laevis cDNA clone XLO91118 3', mRNA sequence.
 ACCESSION BJ088070
 VERSION BJ088070.1 GI:17585186
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 REFERENCE 1 (bases 1 to 625)
 AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 The information of this clone is available through the following
 URL.
 http://xenopus.nibb.ac.jp

FEATURES
source

1. .625
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XLO91118"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_lib="NIBB Mochii normalized Xenopus tailbud
 library"

ORIGIN

Query Match 19.1%; Score 49.4; DB 3; Length 625;
 Best Local Similarity 68.7%; Pred. No. 0.026;
 Matches 68; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

```

Qy 1 CAGCGGAGTGTGGCAAGCACGACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
343 CAAAGACGATATAGACACGACCTTAGAATCTGGAATGCTCAGCTTATTCGCTATGCT 402
Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCT 99
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
403 CGATACAAACAGCCTGATGGTTCGGTCTGGGAGACCCCT 441

RESULT 32
FR0038157
LOCUS FR0038157 619 bp DNA linear GSS 25-FEB-2004
DEFINITION Fugu rubripes GSS sequence, clone 064007cF6, genomic survey
sequence.
ACCESSION AL125658
VERSION AL125658.1 GI:6107273
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
1
REFERENCE
AUTHORS Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrana,Y., Williams,G. and
Brenner,S.
TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
JOURNAL Genome Res. 9 (10), 960-971 (1999)
PUBMED 10523524
REFERENCE
AUTHORS 2 (bases 1 to 619)
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrana,Y., Williams,G. and Brenner,S.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk
COMMENT Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
source
1..619
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="064007cF6"
/clone_lib="cosmid 064007"

ORIGIN
Query Match 18.8%; Score 48.6; DB 11; Length 619;
Best Local Similarity 75.0%; Pred. No. 0.041;
Matches 60; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCACGACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
409 CCGAGGACAGATGGCAACATGACTTTCGATGTGGACATCAGCTGATTCTGTTATGCT 468
Qy 61 GGCTACCAAGATGCCAGATGG 80
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
469 GGGTACAAACAGCCNGATGG 488

RESULT 33
DQ045248
LOCUS DQ045248 3449 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes NOS3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ045248
VERSION DQ045248.1 GI:66896463

```

```

KEYWORDS GSS. troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 3449)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
JOURNAL 15869325
PUBMED
REFERENCE
AUTHORS 2. (bases 1 to 3449)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source
1..3449
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..3449
/clone="NOS3"
/locus_tag="HCL1004"

ORIGIN
Query Match 18.1%; Score 46.8; DB 11; Length 3449;
Best Local Similarity 65.1%; Pred. No. 0.16;
Matches 69; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCACGACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
539 CAGCGCTGCCCTGGCGGAGGAGACTTCCGAATCTGGAACAGCAGCTGTCGCTACGCG 598
Qy 61 GGCTACCAAGATGCCAGATGCCAGCATCAGAGGGGACCCCTGCCACG 106
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
599 GGCTACCGGACGAGGACGCTCTGTGCGGGGAGCCAGCCACG 644

RESULT 34
CK016997
LOCUS AGENCOURT.16541419 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7044445
DEFINITION 5', mRNA sequence.
ACCESSION CK016997
VERSION CK016997.1 GI:38542516
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 906)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LIA014805 row: 1 column: 11
 High quality sequence stop: 626.
 Location/Qualifiers

FEATURES.

source

```
1..906
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:704445"
/tissue_type="whole body"
/lab host="DH10B"
/clone_lib="NIH ZGC 10"
/Note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV; Bulk tissue was collected from a whole adult individual from the Tubingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH_ZGC_7). Library was constructed by Open Biosystems (Huntsville, AL)."
```

ORIGIN

```
Query Match 17.5%; Score 45.2; DB 7; Length 906;
Best Local Similarity 66.3%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 25 TTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCTGGCTACCGATGCCAGATGCCAGC 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 TTTCCCGTGTGGACGCTGAGCTGATAAAGTATGCTGCTATCAGATGGATGGTAGT 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 85 ATCAGAGGGACCCCTGCCAACGCTGGAATTCACTCAGGT 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 740 GTGATCGGCAGCCGCCGCGGTAGACTTTACACAGGT 777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 35

```
BU425320
LOCUS 603961089F1 CSEQBN09 Gallus gallus cdna clone CHEST936a24 5', mRNA
DEFINITION
sequence.
ACCESSION BU425320
VERSION BU425320.1 GI:25917996
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 688)
AUTHORS Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr Biol. 12 (22), 1965-1969 (2002)
PUBMED 1244392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
```

FEATURES

source

```
1..688
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST936a24"
/sex="Male and female"
```

```
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev stage="adult"
/lab host="DH10B"
/clone_lib="CSEQBN09"
/Note="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
```

ORIGIN

```
Query Match 16.7%; Score 43.2; DB 5; Length 688;
Best Local Similarity 75.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 54; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 51 CCGCTATGCTGGCTACCGATGCCAGATGCCAGATGCCAGGGGACCTGCCAACGTGGA 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 CCGATATGCTGGATATCAATGCCAGATGGGTCTGTCATAGGAGACCTGCCAAGTGTGGA 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 111 ATTCACCTCAGGT 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GTTCACAAAGTT 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 36

```
DR123141
LOCUS 49091370 Drosophila pseudoobscura embryonic cDNA library Drosophila pseudoobscura cdna clone K7 5', mRNA sequence.
DEFINITION
ACCESSION DR123141
VERSION DR123141.1 GI:67839839
KEYWORDS EST.
SOURCE Drosophila pseudoobscura
ORGANISM Drosophila pseudoobscura
REFERENCE 1 (bases 1 to 1171)
AUTHORS Richards,S., Liu,Y., Bettencourt,B.R., Hradecky,P., Letovsky,S., Nielsen,R., Thornton,K., Hubisz,M.J., Chen,R., Meisel,R.P., Couronne,O., Hua,S., Smith,M.A., Zhang,P., Liu,J., Bussemaker,H.J., van Batenburg,M.F., Howells,S.L., Scherer,S.E., Sodergren,E., Matthews,B.B., Crosby,M.A., Schroeder,A.J., Ortiz-Barrientos,D., Rives,C.M., Metzker,M.L., Muzny,D.M., Scott,G., Steffen,D., Wheeler,D.A., Worley,K.C., Havlak,P., Durbin,K.J., Egan,A., Gill,R., Hume,J., Morgan,M.B., Miner,G., Hamilton,C., Huang,Y., Waldron,L., Verduzco,D., Clerc-Blankenburg,K.P., Dubchak,I., Noor,M.A., Anderson,W., White,K.P., Clark,A.G., Schaeffer,S.W., Gelbart,W., Weinstock,G.M. and Gibbs,R.A.
```

Comparative genome sequencing of *Drosophila pseudoobscura*: chromosomal, gene, and cis-element evolution
 Genome Res. 15 (1), 1-18 (2005)

JOURNAL

PUBMED

COMMENT

Contact: Stephen Richards
 Human Genome Sequencing Center
 Baylor College of Medicine
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713-798-6667
 Email: stephenr@bcm.tmc.edu

NCBI Trace Archive: 22669760
 Insert Length: 1750 Std Error: 0.25.

FEATURES

source

1..1171

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dt priming from poly A+ RNA, directionally cloned"

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Best Local Similarity 52.9%; Pred. No. 1.9;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 34 TGGAAATGCTAGCTATCGGTATGCTGGTACAGATGCCAGATGGCAGCATCAGAGGG 93
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Db 789 TGGAGTCCCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 848
|||||

Qy 94 GACCTGCCACAGTGGAAATTCACCTCAGGTACCGCGCCAGCCTCAGCCCGGCATTGG 153
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Db 849 GACCCCGCAGCGCCGCCAAACATATCTCGGGCCCAAGCGGACCCCGGTGGACCT 908
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Qy 154 GCGGGGAGCCCGGTGGTGGAGAGTGCAGAGTGGAGCCCGCAGAGGACAC 205
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Db 909 CGCGGCGTTCCTCCGTTGTCGAAGCGGAACCCCTGTTGGACCCAGCGCGCTAC 960
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RESULT 37
DN757217/c
LOCUS
DEFINITION
GL-Cf-14015 GLGC-LIB0001-of Canis familiaris Normalized Mixed
Tissue cDNA Library Canis familiaris cDNA, mRNA sequence.
DN757217
VERSION
DN757217.1 GI:62146330
KEYWORDS
EST.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 567)
AUTHORS
Liu, Q.
TITLE
Direct Submission Gene Logic Inc
JOURNAL
Unpublished (2005)
COMMENT
Contact: Qing Liu
Gene Logic Inc.
610 Professional Drive, Gaithersburg, MD 20879, USA
Tel: 301 987 1700
Email: qlu@genelogic.com.
FEATURES
source
Location/Qualifiers
1..567
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/lab_hosts="EMPH10B"
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Mixed Tissue cDNA Library"
/notes="Organ: heart, liver, kidney, testis, and brain;
Vector: pCMVSPORT6.0; Site_1: NotI; Site_2: SalI"

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Matches 89; Conservative 0; Mismatches 71; Indels 4; Gaps 1;

Qy 39 TGCTCAGCTATCGCTATGCTGCTACCATGCCAGATGCCAGATCAGAGGGGACCC 98
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Db 206 TCCTCAGCGCAGCACCTTTCTTGGGGACCATGCTCAGGGGCTGGCTGGAGCTAGCAGAAC 147
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Qy 99 TGCCAAGTGGAAATTCACCTCAGGTACCCGGCCAGCC----TCAGCCRCGCGGCATTGGG 154
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Db 146 TGCACACGGGAGCCCACTCCGGAAGCCTTNNCCACCGGNNCTGGCTCGGGGATTGGC 87
Qy 155 GCGGGGAGCCCGCTGGTGAGCGAGTGACAGAGTGGAGCCCAAG 198
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Db 86 TCTGGGAGCCCGCTTGGGGGTGGGGGGTGGCCNNNNNNNNCNGNG 43
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RESULT 38
AJ394075/c
LOCUS
DEFINITION
AJ394075 dkfz426 Gallus gallus cDNA clone 17p11r1, mRNA sequence.
ACCESSION
AJ394075
VERSION
AJ394075.1 GI:7123604
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 797)
AUTHORS
Adraakmanov, I., Lodygin, D., Gerth, P., Arakawa, H., Law, A.,
Plachy, J., Korn, B. and Buerstedde, J.M.
TITLE
A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL
Genome Res. 10 (12), 2062-2069 (2000)
PUBMED
11116100
COMMENT
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institut
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
FEATURES
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Location/Qualifiers
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/dev_stage="2-3 weeks old"
/clone_lib="dkfz426"

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Matches 98; Conservative 1; Mismatches 99; Indels 0; Gaps 0;

Qy 14 GCAAGCAGCACTTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCTGGCTACCAATGC 73
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Db 498 GCAGCCACCACTGCCAGCAGCTGCTCTCTCTGTCGCCATGCTGCGTGGAGCGGC 439
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Qy 74 CAGATGGCAGCATCAGAGGGGACCTCGCCAAACGTTGGAATTCACCTCAGGTACCCGGCCAG 133
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Db 438 TTCCTCGTGGAGGAGCTTTGACCCCTCCGAGGAGCGGCACAGACACCTGCACAG 379
|||||

Qy 134 CCTCAGCCRCGCGCATTTGGGGCGGGAGCCCGCTGGTGGAGTGCAGAGTGGAGCC 193
|||||
Db 378 CCAGCGCCACTGCACAGCAGCGCTGAGCACCAGCTGCCAGGAATGCCAGTGGGAAGCA 319
|||||

Qy 194 CAGAGGAGACAGCAGCC 211
Db 318 CTCAGTCAACACCTGCC 301
|||||

RESULT 39
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LOCUS
DEFINITION
UI-M-HB0-cow-f-04-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
IMAGE:30648603 5', mRNA sequence.
ACCESSION
CN459880
VERSION
CN459880.1 GI:46465606
KEYWORDS
EST.
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Beloniformes; Adrianiichthyidae; Oryziinae; Oryzias.
1 (bases 1 to 721)
Kohara, Y., Shin-i.R., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute Of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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            /tissue type="whole embryo"
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            /clone_lib="MF015DA CDNA"

ORIGIN
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Best Local Similarity 67.9%; Pred.No.11;
Matches 55; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy    42 TCAGCTCATCCGTTATCGTGGCTACCAAGATGCCAGATGCAGCATCAGAGGGGACCCTGC 101
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     5 TCAGCTGATTTCGTTACGCAGGTTACAACAGCCTTGACGGACAGATCCTGGAGACCCCGC 64
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy    102 CAACGTGGAATTCACTCAGGT 122
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Db     65 CAATGTGGAGTTCACAGAGAT 85
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Search completed: December 13, 2005, 18:11:36
Job time : 3764 secs

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SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 771) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: Dr. James Lin University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
REFERENCE	Seq primer: pyX-5.
AUTHORS	Location/Qualifiers
TITLE	1. 771
JOURNAL	/organism="Mus musculus"
COMMENT	/mol_type="mRNA" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:30648603" /tissue_type="whole eye" /dev_stage="embryo 12.5,13.5,14.5 dpc" /lab_host="DH10B (T1 phage resistant)" /clone_lib="NIH BMAP HB0" /notes="Organ: Eye; Vector: pyX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
FEATURES	source

ORIGIN							
	Query Match	15.3%	Score 39.6;	DB 7;	Length 771;		
	Best Local Similarity	66.3%;	Pred. No. 10;				
	Matches 57; Conservative	0;	Mismatches 29;	Indels 0;	Gaps 0;		
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Dd	683	CAGCGTCTGCCGCGGGAGACTTCGGATCTGGAAACAGCCAGCTGTACGCTATGCG	742				
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Qy	61	GGCTACCAGATGCCAGATGGCAGCAT	86				
Dd	743	GGCTATAGGCAGCAGGATGGCTCCGT	768				

RESULT 40	
BJ733387	
LOCUS	721 bp mRNA linear EST 09-MAR-2004
DEFINITION	BJ733387 MF015DA cDNA <i>Oryzias latipes</i> cDNA clone MF015DA022j07 5', mRNA sequence.
ACCESSION	BJ733387
VERSION	BJ733387.1 GI:45300699
KEYWORDS	EST.
SOURCE	<i>Oryzias latipes</i> (Japanese medaka)
ORGANISM	<i>Oryzias latipes</i>
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
	Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

SOURCE ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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FEATURES

ORIGIN

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 16:17:25 ; Search time 142 seconds
(without alignments)
3229.654 Million cell updates/sec

Title: US-10-713-137-1
Perfect score: 258
Sequence: 1 cagggagtgatggcaagca.....ttgttccccagctgtgcatc 258

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	257.6	99.8	47420	3	US-09-949-016-15484
3	120.4	46.7	3853	3	US-09-949-016-3742
4	120.4	46.7	3855	3	US-09-949-016-99
5	120.4	46.7	4062	3	US-09-126-109-11
6	120.4	46.7	4062	3	US-09-016-434-1478
7	120.4	46.7	4145	2	US-08-314-917-1
8	120.4	46.7	4145	2	US-08-265-046-1
9	120.4	46.7	4145	2	US-08-465-522-1
10	120.4	46.7	4145	6	PCT-US93-11401-1
11	120.4	46.7	4145	6	PCT-US95-07849-1
12	120.4	46.7	4164	3	US-09-023-655-1407
13	91.6	35.5	4041	2	US-08-147-812-4
14	91.6	35.5	4110	3	US-09-123-708-1
15	91.6	35.5	4110	3	US-09-123-624-1
16	91.6	35.5	4165	2	US-08-147-812-6
17	78.2	30.3	4079	3	US-09-016-434-1477
18	78.2	30.3	4353	2	US-08-365-486A-18
19	78.2	30.3	4353	3	US-08-880-342-18
20	75.6	29.3	5057	2	US-08-365-486A-12
21	75.6	29.3	5057	3	US-08-880-342-12
22	75.6	29.3	5108	2	US-07-642-002-1
23	75	29.1	4780	2	US-08-365-486A-20
24	75	29.1	4780	3	US-09-123-708-3

25	75	29.1	4780	3	US-09-123-624-3	Sequence 3, Appli
26	75	29.1	4780	3	US-08-880-342-20	Sequence 20, Appli
27	56.4	21.9	9208	3	US-09-068-506-1	Sequence 1, Appli
28	54.8	21.2	3612	3	US-09-068-506-2	Sequence 2, Appli
29	54.8	21.2	3690	3	US-09-016-434-1234	Sequence 1234, Ap
30	54.8	21.2	4035	3	US-09-016-434-1369	Sequence 1369, Ap
31	54.8	21.2	4099	3	US-08-896-053-5	Sequence 5, Appli
32	51.6	20.0	4097	3	US-09-123-708-5	Sequence 5, Appli
33	51.6	20.0	4097	3	US-09-123-624-5	Sequence 25, Appli
34	51.6	20.0	4491	3	US-08-809-917-25	Sequence 25, Appli
35	51.6	20.0	4491	3	US-09-419-371-25	Sequence 1, Appli
36	50	19.4	4089	2	US-07-908-245-1	Sequence 17, Appli
37	35.4	13.7	4603	2	US-08-258-261B-17	Sequence 17, Appli
38	35.4	13.7	4603	2	US-08-456-837-17	Sequence 17, Appli
39	35.4	13.7	4603	2	US-08-457-342-17	Sequence 17, Appli
40	35.4	13.7	4603	2	US-08-457-646A-17	Sequence 17, Appli
41	35.4	13.7	4603	2	US-08-458-076A-17	Sequence 17, Appli
42	35.4	13.7	4603	2	US-08-457-335A-17	Sequence 17, Appli
43	35.4	13.7	4603	2	US-08-729-214-17	Sequence 17, Appli
44	35.4	13.7	4603	3	US-09-028-934-17	Sequence 17, Appli
45	35.4	13.7	5698	2	US-08-761-258-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-11841
; Sequence 11841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11841
; LENGTH: 47419
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11841

Query Match	99.8%;	Score 257.6;	DB 3;	Length 47419;
Best Local Similarity	99.6%;	Pred. No. 7e-62;		
Matches 257;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGCGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT	60	
Db	21312	CAGCGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT	21371	
QY	61	GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG	120	
Db	21372	GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG	21431	
QY	121	GTACCCGGCCACGCTCAGCCCGGGGAGCCCGCTGGTGTGAGCGAGTG	180	
Db	21432	GTACCCGGCCACGCTCAGCCCGGGGAGCCCGCTGGTGTGAGCGAGTG	21491	
QY	181	ACAGAGTGGAGCCAGAGGAGACACGACGCCCGGGCTTACAGACTCAGAGGGCCGCTTT	240	
Db	21492	ACAGAGTGGAGCCAGAGGAGACACGACGCCCGGGCTTACAGACTCAGAGGGCCGCTTT	21551	
QY	241	GTTCCTCCAGCTGTGCATC	258	


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Db 21552 GTTCCCGAGCTGTGCATC 21569

RESULT 2
US-09-949-016-15484
; Sequence 15484, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15484
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15484

Query Match 99.8%; Score 257.6; DB 3; Length 47420;
Best Local Similarity 99.6%; Pred. No. 7e-62; Indels 0; Gaps 0;
Matches 257; Conservative 1; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 21312 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 21371
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 21372 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 21431
Qy 121 GTATCCCGGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGCTGGTGAGCCGAGTG 180
Db 21432 GTATCCCGGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGCTGGTGAGCCGAGTG 21491
Qy 181 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAGAGGCCCGCTTT 240
Db 21492 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAGAGGCCCGCTTT 21551
Qy 241 GTTCCCGAGCTGTGCATC 258
Db 21552 GTTCCCGAGCTGTGCATC 21569

RESULT 3
US-09-949-016-3742
; Sequence 3742, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3742

; LENGTH: 3853
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3742

Query Match 46.7%; Score 120.4; DB 3; Length 3853;
Best Local Similarity 99.2%; Pred. No. 5.6e-24; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058
Qy 121 GT 122
Db 1059 CT 1060

RESULT 4
US-09-949-016-99
; Sequence 99, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 3855
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-99

Query Match 46.7%; Score 120.4; DB 3; Length 3855;
Best Local Similarity 99.2%; Pred. No. 5.6e-24; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058
Qy 121 GT 122
Db 1059 CT 1060

RESULT 5
US-09-126-109-11
; Sequence 11, Application US/09126109
; Patent No. 6171856
; GENERAL INFORMATION:
; APPLICANT: Thigpen, Anice
; APPLICANT: Hohmeier, Hans-Ewald
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Unger, Roger H.
```

APPLICANT: Shimabukuro, Michio
 APPLICANT: Chen, Guaxun
 APPLICANT: Rhodes, Christopher J.
 APPLICANT: Hugl, Sigrun R.
 APPLICANT: Cousin, Sharon
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
 TO NO-MEDIATED CVTOTOXICITY
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/126,109
 FILING DATE: 30-JUL-1998
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/055,092
 FILING DATE: 30-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US Unknown
 FILING DATE: 03-MAR-1998

ATTORNEY/AGENT INFORMATION:
 NAME: McMillian, Nabeela R.
 REGISTRATION NUMBER: P-43,363
 REFERENCE/DOCKET NUMBER: USD:560
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4062 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-126-109-11

Query Match 46.7%; Score 120.4; DB 3; Length 4062;
 Best Local Similarity 99.2%; Pred. No. 5.7e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 850 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACAGATGCCAGATGCGCAGATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
 DB 910 GGCTACAGATGCCAGATGCGCAGATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 969

QY 121 GT 122
 DB 970 CT 971

RESULT 6
 US-09-016-434-1478
 Sequence 1478, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016.434
 FILING DATE: HEREWITH
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1478:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4062 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9951320
 US-09-016-434-1478

Query Match 46.7%; Score 120.4; DB 3; Length 4062;
 Best Local Similarity 99.2%; Pred. No. 5.7e-24;
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
 DB 850 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACAGATGCCAGATGCGCAGATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
 DB 910 GGCTACAGATGCCAGATGCGCAGATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 969

QY 121 GT 122
 DB 970 CT 971

RESULT 7
 US-08-314-917-1
 Sequence 1, Application US/08314917
 Patent No. 5486630
 GENERAL INFORMATION:
 APPLICANT: Billiar, Timothy R.
 APPLICANT: Nussler, Andreas K.
 APPLICANT: Geller, David A.
 APPLICANT: Simmons, Richard L.
 TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
 TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold B. Silverman
 ADDRESSEE: Eckert Seamans Cherin & Mellott
 STREET: 600 Grant Street, 42nd Floor
 CITY: Pittsburgh
 STATE: PA

```
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/314,917
; APPLICATION NUMBER: US/08/314,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-314-917-1

Query Match 46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010

Qy 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 1070

Qy 121 GT 122
Db 1071 CT 1072

RESULT 8
US-08-265-046-1
; Sequence 1, Application US/08265046
; Patent No. 5658565
; GENERAL INFORMATION:
; APPLICANT: Timothy R. Billiar
; APPLICANT: Edith Tzeng
; APPLICANT: Andreas K. Nussler
```

```
; APPLICANT: David A. Geller
; APPLICANT: Richard L. Simmons
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,046
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Lewis F. Jr.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 119130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-265-046-1

Query Match 46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGCGAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010

Qy 61 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 1070

Qy 121 GT 122
Db 1071 CT 1072
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RESULT 9
US-08-465-522-1
; Sequence 1, Application US/08465522
; Patent No. 5882908
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market St. Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,522
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 116972-6
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; DESCRIPTION: Synthase cDNA Clone
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
US-08-465-522-1
Query Match 46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGCAGACGACGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGCAGACGACGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
Qy 61 GGCTACCATGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAAGCTGGAAATTCATCTCAG 120
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1011 GGCTACCATGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAAGCTGGAAATTCATCTCAG 1070
Qy 121 GT 122
Db 1071 CT 1072
RESULT 10
PCT-US93-11401-1
; Sequence 1, Application PCTUS9311401
; GENERAL INFORMATION:
; APPLICANT: Billiar, Timothy R.
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard L.
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold B. Silverman
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 600 Grant Street, 42nd Floor
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11401
; FILING DATE: 25-NOV-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
PCT-US93-11401-1
Query Match 46.7%; Score 120.4; DB 6; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 970 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029

Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120

Db 1030 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 1089

Qy 121 GT 122

Db 1090 CT 1091

RESULT 13

US-08-147-812-4

Sequence 4, Application US/08147812

Patent No. 5766909

GENERAL INFORMATION:

APPLICANT: Xie, Qiao-wen

APPLICANT: Nathan, Carl F.

APPLICANT: Mumford, Richard A.

APPLICANT: Calaycay, Jimmy Ramos

TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh Centris650

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,812

FILING DATE: No. 5766909 Available

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/841,641

FILING DATE: 02-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, John W III

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 186581A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

TELEX: 138825

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4041 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-147-812-4

Query Match 35.5%; Score 91.6; DB 2; Length 4041;

Best Local Similarity 84.4%; Pred. No. 5.7e-16;

Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 982 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1041

Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120

Db 1042 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 1101

Qy 121 GT 122

Db 1102 TT 1103

RESULT 14

US-09-123-708-1

Sequence 1, Application US/09123708

Patent No. 6146887

GENERAL INFORMATION:

APPLICANT: SCHRAMER, Juergen

APPLICANT: GOEDECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REFERENCE: 511169-2003

CURRENT APPLICATION NUMBER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503

EARLIER FILING DATE: 1996-03-01

EARLIER APPLICATION NUMBER: P4411402.8

EARLIER FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 4110

TYPE: DNA

ORGANISM: Cytomegalovirus

US-09-123-708-1

Query Match 35.5%; Score 91.6; DB 3; Length 4110;

Best Local Similarity 84.4%; Pred. No. 5.8e-16;

Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 918 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 977

Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120

Db 978 GGCTACCAAGATCCGCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTTCAACCAG 1037

Qy 121 GT 122

Db 1038 TT 1039

RESULT 15

US-09-123-624-1

Sequence 1, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:

APPLICANT: SCHRAMER, Juergen

APPLICANT: GOEDECKE, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REFERENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

CURRENT FILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 08/553,503

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: 4411402.8

PRIOR FILING DATE: 1994-03-31

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 4110

TYPE: DNA

ORGANISM: Mus musculus

US-09-123-624-1

Query Match 35.5%; Score 91.6; DB 3; Length 4110;

Best Local Similarity 84.4%; Pred. No. 5.8e-16;

Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 918 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 977

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAACGTGGAAATTCACCTCAG 120
|
Db 978 GGCTACCAGATGCCAGATGCCAGATCAGAGGGAGCTGCTGCCACCTTGGAGTTCAACCAG 1037

QY 121 GT 122
|
Db 1038 TT 1039

RESULT 16

US-08-147-812-6
; Sequence 6, Application US/08147812
; Patent No. 5766909
; GENERAL INFORMATION:
; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycav, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh Centris650
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,812
; FILING DATE: No. 5766909 Available
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/841,641
; FILING DATE: 02-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 186581A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; TELEX: 138825

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-147-812-6

Query Match 35.5%; Score 91.6; DB 2; Length 4165;
Best Local Similarity 84.4%; Pred. No. 5.8e-16;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCAGCACTCCGGGTGTGGAATGCTCAGGCTCATCCGCTATGCT 60
|
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTAGCT 1041

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAACGTGGAAATTCACCTCAG 120
|
Db 1042 GGCTACCAGATGCCAGATGCCAGATCAGAGGGAGCTGCCACCTTGGAGTTCAACCAG 1101

QY 121 GT 122
|
Db 1102 TT 1103

RESULT 17

US-09-016-434-1477
; Sequence 1477, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g951318

US-09-016-434-1477

Query Match 30.3%; Score 78.2; DB 3; Length 4079;
Best Local Similarity 77.2%; Pred. No. 3e-12;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCAGCACTCCGGGTGTGGAATGCTCAGGCTCATCCGCTATGCT 60
|
Db 1412 CAGAGGACAGACGGCAAGCAGCACTCCGAGTCTGGAATCTCCAGGCTCATCCGCTAGCT 1471

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAACGTGGAAATTCACCTCAG 120
|
Db 1472 GGCTAACAGCAGCCTCAGCGCTCCACCTGGGGGACCCAGCCCAATGTGCAGTTTCACAGAG 1531

QY 121 GTA 123
|
Db 1532 ATA 1534

RESULT 18

US-08-365-486A-18
; Sequence 18, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated


```

; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.,
; INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4305
; US-08-365-486A-18

Query Match 30.3%; Score 78.2; DB 2; Length 4353;
Best Local Similarity 77.2%; Pred. No. 3.1e-12;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 1405 CAGAGACAGACGGCAAGCAGCAGCTTCGGAGTCTGGAACTCCAGCTCATCCGCTACGCT 1464

QY 61 GGCTACCATGCGAGATGGCAGCATCAGAGGGGACCTGCGCAAGTGGAAATTCACCTCAG 120
DB 1465 GGCTACAGCAGCTGACGGCTCCACCTTGGGGGACCCAGCCATGTGTCAGTTCACAGAG 1524

QY 121 GTA 123
DB 1525 ATA 1527

RESULT 19
US-08-880-342-18
; Sequence 18, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.,
; INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4305
; US-08-365-486A-18

Query Match 30.3%; Score 78.2; DB 2; Length 4353;
Best Local Similarity 77.2%; Pred. No. 3.1e-12;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 1405 CAGAGACAGACGGCAAGCAGCAGCTTCGGAGTCTGGAACTCCAGCTCATCCGCTACGCT 1464

QY 61 GGCTACCATGCGAGATGGCAGCATCAGAGGGGACCTGCGCAAGTGGAAATTCACCTCAG 120
DB 1465 GGCTACAGCAGCTGACGGCTCCACCTTGGGGGACCCAGCCATGTGTCAGTTCACAGAG 1524

QY 121 GTA 123
DB 1525 ATA 1527

RESULT 20
US-08-365-486A-12
; Sequence 12, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

```

```
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: rat bnOS cdNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 349..4638
; US-08-365-486A-12

Query Match 29.3%; Score 75.6; DB 2; Length 5057;
Best Local Similarity 76.2%; Pred. No. 1.7e-11;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 1738 CAGAGGACTGACGCGCAACATGACTCCGAGTGTGGAACTCGCAGCTCATCCGCTACGCG 1797
Qy 61 GGCTACCAAGCAGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1798 GGCTACCAAGCAGCAGATGCGCTCTACCTTGGGGGATCCAGCCAAATGTGCAGTTCAAGGAG 1857
Qy 121 GT 122
Db 1858 AT 1859

RESULT 21
US-08-880-342-12
; Sequence 12, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: rat bnOS cdNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 349..4638
; US-08-365-486A-12

Query Match 29.3%; Score 75.6; DB 3; Length 5057;
Best Local Similarity 76.2%; Pred. No. 1.7e-11;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 1738 CAGAGGACTGACGCGCAACATGACTCCGAGTGTGGAACTCGCAGCTCATCCGCTACGCG 1797
Qy 61 GGCTACCAAGCAGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1798 GGCTACCAAGCAGCAGATGCGCTCTACCTTGGGGGATCCAGCCAAATGTGCAGTTCAAGGAG 1857
Qy 121 GT 122
Db 1858 AT 1859

RESULT 22
US-07-642-002-1
; Sequence 1, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Brett, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: One Thomas Circle, NW
; CITY: Washington
```

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; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/642,002
; FILING DATE: 19910118
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.033576
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 296-5500
; TELEFAX: (202) 296-7830
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5108 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 400..4686
; OTHER INFORMATION:
;
; US-07-642-002-1
;
; Query Match 29.3%; Score 75.6; DB 2; Length 5108;
; Best Local Similarity 76.2%; Pred. No. 1.7e-11;
; Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
;
; QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; Db 1789 CAGGAGCTACCGGCAACATGACTTCCGAGTGTGGAATGCTCAGCTCATCCGCTACGGC 1848
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 61 GGCTACAGATGCCAGATGCCAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 120
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; Db 1849 GGCTACAGCAGCCAGATGCTCTACTTTGGGGGATCCAGCCAAATGTGCAGTTCACGGAG 1908
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 121 GT 122
; Db 1909 AT 1910
;
; RESULT 23
; US-08-365-486A-20
; Sequence 20, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al,
; INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 431..4732
; US-08-365-486A-20
;
; Query Match 29.1%; Score 75; DB 2; Length 4780;
; Best Local Similarity 75.6%; Pred. No. 2.4e-11;
; Matches 93; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
;
; QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; Db 1832 CAGAGGACAGACGGCAGCAGCAGCTTCCGAGTCTGGAATCTCCAGCTCATCCGCTACGCT 1891
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 61 GGCTACAGATGCCAGATGCCAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 120
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; Db 1892 GGCTACAAAGCACCGTGACGGCTCCACCTTGGGGGACCCAGCCAAATGTGCAGTTCACAG 1951
; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; QY 121 GTA 123
; Db 1952 ATA 1954
;
; RESULT 24
; US-09-123-708-3
; Sequence 3, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Cytomegalovirus
; US-09-123-708-3
;
; Query Match 29.1%; Score 75; DB 3; Length 4780;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: nnnnnnnnn = Intervening sequences of introns
US-09-068-506-1

Query Match      21.9%; Score 56.4; DB 3; Length 9208;
Best Local Similarity 66.4%; Pred. No. 4.1e-06;
Matches 81; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3172 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCAGCTGGTGGCTACGGG 3231

QY 61 GGTACACAGATGCAGATGCCAGCATCAGAGGGGACCTTGCCAAAGTGGAAATTCATCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3232 GGTACCGGCAGCAGGACGGCTCTGTGCGGGGGGACCCAGGCCAACGTTGGAGATCACCGAG 3291

QY 121 GT 122
    ||
Db 3292 GT 3293

RESULT 28
US-09-068-506-2
; Sequence 2, Application US/09068506A
; Patent No. 6569618
; GENERAL INFORMATION:
; APPLICANT: YASUE, Hirofumi
; APPLICANT: YOSHIMURA, Kumamoto
; TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
; TITLE OF INVENTION: TWITCHING
; FILE REFERENCE: 0032-245P
; CURRENT APPLICATION NUMBER: US/09/068,506A
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-068-506-2

Query Match      21.2%; Score 54.8; DB 3; Length 3612;
Best Local Similarity 65.6%; Pred. No. 9.4e-06;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCAGCTGGTGGCTACGGG 756

QY 61 GGTACACAGATGCAGATGCCAGCATCAGAGGGGACCTTGCCAAAGTGGAAATTCATCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 757 GGTACCGGCAGCAGGACGGCTCTGTGCGGGGGGACCCAGGCCAACGTTGGAGATCACCGAG 816

QY 121 GT 122
    ||
Db 817 CT 818

RESULT 29
US-09-016-434-1234
; Sequence 1234, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1234:
SEQUENCE CHARACTERISTICS:
LENGTH: 3690 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g189259
US-09-016-434-1234

Query Match      21.2%; Score 54.8; DB 3; Length 3690;
Best Local Similarity 65.6%; Pred. No. 9.5e-06;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCAGCTGGTGGCTACGGG 776

QY 61 GGTACACAGATGCAGATGCCAGCATCAGAGGGGACCTTGCCAAAGTGGAAATTCATCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 777 GGTACCGGCAGCAGGACGGCTCTGTGCGGGGGGACCCAGGCCAACGTTGGAGATCACCGAG 836

QY 121 GT 122
    ||
Db 837 CT 838

RESULT 30
US-09-016-434-1369
; Sequence 1369, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; CLASSIFICATION:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1369:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9434699
US-09-016-434-1369

Query Match 21.2%; Score 54.8; DB 3; Length 4035;
Best Local Similarity 65.6%; Pred. No. 9.7e-06;
Matches 80; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 748 CAGCGCTGCCCTGGCCGAGGAGACTTCGGAATCTGGAACAGCCAGCTGGTGCGCTACGCG 807

Qy 61 GGCTACCATGTCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 808 GGCTACCGGCAGCAGGAGCGGCTCTGTGCGGGGGACCCAGCCACAGCTGGAGATCACCAG 867

Qy 121 GT 122
Db 868 CT 869

RESULT 31
US-08-896-053-5
; Sequence 5, Application US/08896053
; Patent No. 6720309
; GENERAL INFORMATION:
; APPLICANT: Janssens, Stefans
; APPLICANT: Bloch, Kenneth D.
; APPLICANT: Collen, D sir
; TITLE OF INVENTION: Method of Inducing Vasodilation and
; TITLE OF INVENTION: Treating Pulmonary Hypertension Using Adenoviral-Mediated
; TITLE OF INVENTION: Transfer of the Nitric Oxide Synthase Gene
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896.053
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; FILING DATE: 17-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,912
; FILING DATE: 17-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Millonig, Robert C.
; REGISTRATION NUMBER: 34,395
; REFERENCE/DOCKET NUMBER: 0609.4280001/JAG/RCM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4099 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-896-053-5

Query Match 21.2%; Score 54.8; DB 3; Length 4099;
Best Local Similarity 65.6%; Pred. No. 9.7e-06;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 743 CAGCGCTGCCCTGGCCGAGGAGACTTCGGAATCTGGAACAGCCAGCTGGTGCGCTACGCG 802

Qy 61 GGCTACCATGTCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 803 GGCTACCGGCAGCAGGAGCGGCTCTGTGCGGGGGACCCAGCCAACTGGAGATCACCAG 862

Qy 121 GT 122
Db 863 CT 864

RESULT 32
US-09-123-708-5
; Sequence 5, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4097
; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-5

Query Match 20.0%; Score 51.6; DB 3; Length 4097;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 760 CAGCGCGCCCGCGCGGAGACTTCGGGATCTGGAACAGCCAGCTGGTGCGCTACGCA 819

Qy 61 GGCTACCATGTCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 820 GGCTACAGACAGCAGGATGGCTCTGTGCGTGGGGACCCAGCCAACTGGAGATCACCAG 879
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QY 121 GTACCGGCC 130
DB 880 CTCTGCATCC 889

RESULT 33
US-09-123-624-5
; Sequence 5, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRAEDER, Jurgen
; APPLICANT: CODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 51169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4097
; TYPE: DNA
; ORGANISM: Bos taurus
US-09-123-624-5

Query Match 20.0%; Score 51.6; DB 3; Length 4097;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTATCGCTATGCT 60
DB 760 CAGCGGCGCCCGCGCGGAGACTTCGGATCTGGAACAGCCAGCTGGTGGCTACGCA 819

QY 61 GGTACAGATGCAGATGCGAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCTAG 120
DB 820 GGCTACAGACAGCAGGATGGCTGTGGTGGGGGCCAGCCAGCAACGTGGAGATCACGGAG 879

QY 121 GTACCGGCC 130
DB 880 CTCTGCATCC 889

RESULT 34
US-08-809-917-25
; Sequence 25, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM type: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,917
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13198
; FILING DATE:
; APPLICATION NUMBER: US 08/361,063
; FILING DATE: 21-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,866
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4491 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-809-917-25

Query Match 20.0%; Score 51.6; DB 3; Length 4491;
Best Local Similarity 63.9%; Pred. No. 7.6e-05;
Matches 78; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTATCGCTATGCT 60
DB 1320 CAACGACAGATGCCAAGCATGATTATCGCATTTTGGGAATAACCAATTATATCTTATGCC 1379

QY 61 GGTACAGATGCAGATGCGAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCTAG 120
DB 1380 GGCTACAGACAGCGCGGATGGAAAATCATTTGGCGATCCCATGAATGTGGAGTTACAGAG 1439

QY 121 GT 122
DB 1440 GT 1441

RESULT 35
US-09-419-371-25
; Sequence 25, Application US/09419371
; Patent No. 6890516
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry Chi-Ping
; TITLE OF INVENTION: Cloning and Characterizing of Genes
; TITLE OF INVENTION: Associated With Long-Term Memory
; FILE REFERENCE: CSHL94-03A3Z
; CURRENT APPLICATION NUMBER: US/09/419,371
; CURRENT FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 08/809,917
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: PCT/US95/13198
; PRIOR FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: 08/361,063
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/319,866
; PRIOR FILING DATE: 1994-10-07
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 4491
; TYPE: DNA
; ORGANISM: Drosophila
US-09-419-371-25

Query Match 20.0%; Score 51.6; DB 3; Length 4491;
Best Local Similarity 63.9%; Pred. No. 7.6e-05;
Matches 78; Conservative 0; Mismatches 44; Indels 0; Gaps 0;


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Qy 1 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 1320 CAAGCCAGATGCCAAGCATGATTATCGCATTTGGAAATACCAATTAATCTTATGCC 1379

Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACATCAG 120
Db 1380 GGCTACAAGCAGCGGATGGAAATATCATTGGCGATCCATGAATGTGGAGTTTACAGAG 1439

Qy 121 GT 122
Db 1440 GT 1441

RESULT 36
US-07-908-245-1
; Sequence 1, Application US/07908245
; Patent No. 5498539
; GENERAL INFORMATION:
; APPLICANT: Harrison, David G.
; APPLICANT: Alexander, R. Wayne
; APPLICANT: Murphy, T.J.
; APPLICANT: Nishida, Ken'ichi
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,245
; FILING DATE: 19920702
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU 111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4089 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; TISSUE TYPE: Aorta
; CELL TYPE: Endothelial
US-07-908-245-1
Query Match 19.4%; Score 50; DB 2; Length 4089;
Best Local Similarity 61.5%; Pred. No. 0.00021;
Matches 80; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 732 CAGCGCGCCCGCGCGGAGATTCGCGATCTTGGAAACAGCAGCTGGTGGCTACGCA 791

Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACATCAG 120
Db 792 GGCTACACAGACAGCAGGATGGCTCTGTGCTGGGGACCCAGCCAAATGTGGAGATCACGGAG 851
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Qy 121 GTACCCGGCC 130
Db 852 CTCTGCATCC 861
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RESULT 37
US-08-258-261B-17/C
; Sequence 17, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gafney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hamner, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..1594
; OTHER INFORMATION: /gene= "phz1"
; OTHER INFORMATION: /label= ORF1
; OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1598..2758
; OTHER INFORMATION: /gene= "phz2"
; OTHER INFORMATION: /label= ORF2
; OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2764..3597
; OTHER INFORMATION: /gene= "phz3"
; OTHER INFORMATION: /label= ORF3
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; OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3597..4262
; OTHER INFORMATION: /label= ORF4
; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This information is repeated in SEQ ID NO:21 due to overlapping ORFs."
; OTHER INFORMATION: is repeated in SEQ ID NO:21 due to overlapping ORFs."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4603
; OTHER INFORMATION: /note= "Four open reading frames"
; OTHER INFORMATION:
; OTHER INFORMATION: Example 18 of the specification."
;
US-08-258-261B-17

Query Match 13.7%; Score 35.4; DB 2; Length 4603;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 169 CACCGCAGTAATGCTTGCCACGGGTTTCAGCGCGGGTTCGACAGGGCTTTTGTAGCGGCT 110

Qy 61 GGTACCATGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGG 109
Db 109 GGCACCTGATCAGCGCGCGGCGGATCGGAAGCGCACTCGCTGACGTCG 61

RESULT 38
US-08-456-837-17/c
; Sequence 17, Application US/08456837
; Patent No. 5643774
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas M.
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,837
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689

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	Query Match	13.7%	Score 35.4;	DB 2;	Length 4603;
	Best Local Similarity	57.8%;	Pred. No. 2.4;		
	Matches 63;	Conservative 0;	Mismatches 46;	Indels 0;	Gaps 0;
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Db	169	CACGCGAGTAATGGCTTTGCCAGGGGTTTCAGCGCGGGTTCGCACAGGCTTTTGTAGCGGCT	110		
Qy	61	GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGG	109		

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;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3597..4262
; OTHER INFORMATION: /label= ORF4
; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This information is repeated in SEQ ID NO:21 due to overlapping ORFs."
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4603
; OTHER INFORMATION: /note= "Four open reading frames
; OTHER INFORMATION:
; OTHER INFORMATION: Example 18 of the specification."
;
US-08-457-646A-17
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Query Match 13.7%; Score 35.4; DB 2; Length 4603;
Best Local Similarity 57.8%; Pred. No. 2.4; Mismatches 46; Indels 0; Gaps 0;
Matches 63; Conservative 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
   |||||
Db 169 CACCGCAGTAATGGCTTGCAGGGGTTCAAGGCGGGTGCACAGGCTTTTGTAGCGGCT 110
   |||||

QY 61 GGCTACCGAGATGCCAGATGGCAGCATCAGAGGGACCTGCCCAACGTGG 109
   |||||
Db 109 GGCACCTGATGACGGCGGGCATCGGAGGCGCACCTCGCTGACGTCG 61
   |||||
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Search completed: December 13, 2005, 18:14:07
Job time : 144 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 16:24:48 ; Search time 796 Seconds
(without alignments)
2680.276 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 cagcggagtgatggcaagca.....tgttccccagctgtgcac 258

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	258	US-10-713-137-1	Sequence 1, Appli
2	256.8	99.5	55689	US-10-741-601-5684	Sequence 5684, Ap
3	256.8	99.5	55689	US-10-741-600-17734	Sequence 17734, A
4	200.6	77.8	201	US-10-741-601-19182	Sequence 19182, A
5	200.6	77.8	201	US-10-741-600-51219	Sequence 51219, A
6	200.2	77.6	201	US-10-741-601-19156	Sequence 19156, A
7	200.2	77.6	201	US-10-741-600-51193	Sequence 51193, A
8	191.2	74.1	201	US-10-741-601-19177	Sequence 19177, A
9	191.2	74.1	201	US-10-741-600-51214	Sequence 51214, A
10	120.4	46.7	1152	US-10-220-282A-3	Sequence 3, Appli
11	120.4	46.7	3462	US-10-220-282A-1	Sequence 1, Appli
12	120.4	46.7	3855	US-10-210-682-1	Sequence 1, Appli
13	120.4	46.7	4062	US-10-305-720-1478	Sequence 1478, Ap
14	120.4	46.7	4062	US-10-631-467-38	Sequence 38, Appl
15	120.4	46.7	4062	US-10-631-467-155	Sequence 155, App
16	120.4	46.7	4133	US-10-741-601-228	Sequence 228, App
17	120.4	46.7	4133	US-10-741-600-621	Sequence 621, App
18	120.4	46.7	4145	US-10-182-049-3	Sequence 3, Appli
19	120.4	46.7	4145	US-10-182-049-10	Sequence 10, Appl
20	120.4	46.7	4164	US-10-641-643-1407	Sequence 1407, Ap
21	120.4	46.7	4221	US-10-741-601-229	Sequence 229, App
22	120.4	46.7	4221	US-10-741-600-622	Sequence 622, App
23	118.8	46.0	4150	US-10-688-845-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-10-713-137-1
; Sequence 1, Application US/10713137
; Publication No. US20050106573A1
; GENERAL INFORMATION:
; APPLICANT: Pasha, Abdul Qadar Mohammad
; APPLICANT: Ahsan, Aarif
; TITLE OF INVENTION: A method of detection of predisposition
; TITLE OF INVENTION: to high altitude pulmonary edema (HAPE)
; FILE REFERENCE: 09755-0018US1
; CURRENT APPLICATION NUMBER: US/10/713,137
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Human
US-10-713-137-1

Query Match 99.8%; Score 257.6; DB 9; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAGCGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGATGCTCAGCTCATCGCTATGCT	60
DB	1		60
QY	61	GCTTACCAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACCTGGAAATTCATCTCAG	120
DB	61		120
QY	121	GTATCCCGGCCAGCTCAGCCRCGCCCATTTGGGGGGGGAGCCCGCTGGTAGCCAGTG	180
DB	121		180
QY	181	ACAGAGTGAGGCCAGAGAGACACGACGCCCGGGGTTCACAGCTCAGAGGGCCCGCTTT	240
DB	181		240
QY	241	GTTCGCCAGCTGTGCATC	258
DB	241		258

RESULT 2


```
Query Match 77.8%; Score 200.6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.6e-53;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 101
Db 1 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 60

Qy 102 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 161
Db 61 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 120

Qy 162 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 221
Db 121 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 180

Qy 222 GACTCACAGGGCCCGCTTTGT 242
Db 181 GACTCACAGGGCCCGCTTTGT 201

RESULT 6
US-10-741-601-19156
; Sequence 19156, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19156
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-19156

Query Match 77.6%; Score 200.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.2e-52;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 44 AGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCA 103
Db 1 AGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCA 60

Qy 104 AGCTGGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGAGC 163
Db 61 AGCTGGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGAGC 120

Qy 164 CCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 223
Db 121 CCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 180

Qy 224 CTCACAGGGCCCGCTTTGTTTC 244
Db 181 CTCACAGGGCCCGCTTTGTTTC 201

RESULT 7
US-10-741-600-51193
; Sequence 51193, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997

Query Match 77.8%; Score 200.6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.6e-53;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 101
Db 1 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 60

Qy 102 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 161
Db 61 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 120

Qy 162 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 221
Db 121 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 180

Qy 222 GACTCACAGGGCCCGCTTTGT 242
Db 181 GACTCACAGGGCCCGCTTTGT 201

RESULT 8
US-10-741-601-19177
; Sequence 19177, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19177
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-19177

Query Match 74.1%; Score 191.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 7.5e-50;
Matches 190; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 67 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGAATTCACCTCAGGTACCC 126
Db 1 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGAATTCACCTCAGGTACCC 60

Qy 127 GSCCCAGCCTCAGCCRCGCCGCTTTGGGCGGGGAGCCCGCTGTGTGAGAGTGAAGAG 186
Db 61 GSCCCAGCCTCAGCCRCGCCGCTTTGGGCGGGGAGCCCGCTGTGTGAGAGTGAAGAG 120

Qy 187 TGGAGCCCAAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCCC 246
Db 121 TGGAGCCCAAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCCC 180

Qy 247 CAGCTGTGCATC 258
Db 181 CAGCTGTGCATC 192

RESULT 9
US-10-741-600-51214
; Sequence 51214, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
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Query Match 77.8%; Score 200.6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.6e-53;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 101
Db 1 TCAGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGC 60

Qy 102 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 161
Db 61 CAAGTGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGGA 120

Qy 162 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 221
Db 121 GCCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACA 180

Qy 222 GACTCACAGGGCCCGCTTTGT 242
Db 181 GACTCACAGGGCCCGCTTTGT 201

RESULT 6
US-10-741-601-19156
; Sequence 19156, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19156
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-19156

Query Match 77.6%; Score 200.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.2e-52;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 44 AGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCA 103
Db 1 AGCTATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCA 60

Qy 104 AGCTGGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGAGC 163
Db 61 AGCTGGAATTCACCTAGGTACCGGCCAGCCTCAGCCCGCCATTTGGGCGGGAGC 120

Qy 164 CCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 223
Db 121 CCCGTGTGAGCGAGTGACAGATGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 180

Qy 224 CTCACAGGGCCCGCTTTGTTTC 244
Db 181 CTCACAGGGCCCGCTTTGTTTC 201

RESULT 7
US-10-741-600-51193
; Sequence 51193, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
```

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51214
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-51214

Query Match 74.1%; Score 191.2; DB 8; Length 201;
Best Local Similarity 99.0%; Pred. No. 7.5e-50;
Matches 190; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 67 CAGATGCCAGATGCCAGCATCAGAGGGGACCTGCGCAACGTGGAATTCACCTCAGGTACCC 126
Db 1 CAGATGCCAGATGCCAGCATCAGAGGGGACCTGCGCAACGTGGAATTCACCTCAGGTACCC 60

QY 127 GGGCCAGCCTCAGCCCGCCCATTTGGGGGGGAGCCCGTGGTGAGCGAGTGACAGAG 186
Db 61 GGGCCAGCCTCAGCGCGCGCCATTTGGGGGGGAGCCCGTGGTGAGCGAGTGACAGAG 120

QY 187 TGAGGCCAGAGAGACACCGCCCGGGTTACAGACTCACAGGCGCGCTTTGTTCCC 246
Db 121 TGAGGCCAGAGAGACACCGCCCGGGTTACAGACTCACAGGCGCGCTTTGTTCCC 180

QY 247 CAGCTGTGCATC 258
Db 181 CAGCTGTGCATC 192

RESULT 10
US-10-220-282A-3
; Sequence 3, Application US/10220282A
; Publication No. US20040053323A1
; GENERAL INFORMATION:
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: UEDA, YOSHIKO
; APPLICANT: IWAMI, MORITA
; APPLICANT: ARAKAWA, HIROYUKI
; APPLICANT: NOTSU, YOSHITADA
; TITLE OF INVENTION: SCREENING METHODS FOR INHIBITORS OF INDUCIBLE NITROGEN OXIDE SYNT
; FILE REFERENCE: 227899USOPCT
; CURRENT APPLICATION NUMBER: US/10/220,282A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: PCT/JP01/01865
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-72480
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1152)
; OTHER INFORMATION:
US-10-220-282A-3

Query Match 46.7%; Score 120.4; DB 7; Length 1152;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 379 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 438

QY 61 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 439 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 498

QY 121 GT 122
Db 499 CT 500

RESULT 11
US-10-220-282A-1
; Sequence 1, Application US/10220282A
; Publication No. US20040053323A1
; GENERAL INFORMATION:
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: UEDA, YOSHIKO
; APPLICANT: IWAMI, MORITA
; APPLICANT: ARAKAWA, HIROYUKI
; APPLICANT: NOTSU, YOSHITADA
; TITLE OF INVENTION: SCREENING METHODS FOR INHIBITORS OF INDUCIBLE NITROGEN OXIDE SYNT
; FILE REFERENCE: 227899USOPCT
; CURRENT APPLICATION NUMBER: US/10/220,282A
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: PCT/JP01/01865
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-72480
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3462)
; OTHER INFORMATION:
US-10-220-282A-1

Query Match 46.7%; Score 120.4; DB 7; Length 3462;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 745 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804

QY 61 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 805 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 864

QY 121 GT 122
Db 865 CT 866

RESULT 12
US-10-210-682-1
; Sequence 1, Application US/10210682
; Publication No. US20030092039A1
; GENERAL INFORMATION:
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Donald, Glen
; TITLE OF INVENTION: Screening Nutraceuticals
; FILE REFERENCE: FORS-07289
; CURRENT APPLICATION NUMBER: US/10/210,682
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/309,279
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 1
; LENGTH: 3855
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-210-682-1

Query Match          46.7%; Score 120.4; DB 5; Length 3855;
Best Local Similarity 80.3%; Pred. No. 1.1e-27;
Matches 98; Conservative 23; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 939 CAGCGGAGUGAUGGCAAGCAGCAGCUCUCCGGGUGUGAAUGCUCAGCUCAUCCGCUAUGCU 998

QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 999 GCGUACCAAGAUCCAGAGGAGCAGCAGCAGGAGGGGACCCUGCCAAAGUGGAAUUCACUCAG 1058

QY 121 GT 122
Db 1059 CU 1060

RESULT 13
US-10-305-720-1478
; Sequence 1478, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1478
; TYPE: DNA
; LENGTH: 4062
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g951320
US-10-305-720-1478

Query Match          46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 850 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969

QY 121 GT 122
Db 970 CT 971

RESULT 14
US-10-631-467-38
; Sequence 38, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
```

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; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-631-467-38

Query Match          46.7%; Score 120.4; DB 9; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 850 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969

QY 121 GT 122
Db 970 CT 971

RESULT 15
US-10-631-467-155
; Sequence 155, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 155
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-631-467-155

Query Match          46.7%; Score 120.4; DB 9; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 850 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969

QY 121 GT 122
Db 970 CT 971

RESULT 16
US-10-741-601-228
; Sequence 228, Application US/10741601
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; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-228

Query Match          46.7%; Score 120.4; DB 7; Length 4133;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998

QY 61 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058

QY 121 GT 122
Db 1059 CT 1060

RESULT 17
US-10-741-600-621
; Sequence 621, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-621

Query Match          46.7%; Score 120.4; DB 8; Length 4133;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998

QY 61 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058

QY 121 GT 122
Db 1059 CT 1060

RESULT 18
US-10-182-049-3
; Sequence 3, Application US/10182049
; Publication No. US20050113322A1
```

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; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 3
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)...(3668)
US-10-182-049-3

Query Match          46.7%; Score 120.4; DB 9; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010

QY 61 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070

QY 121 GT 122
Db 1071 CT 1072

RESULT 19
US-10-182-049-10
; Sequence 10, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 10
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(4110)
US-10-182-049-10

Query Match          46.7%; Score 120.4; DB 9; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010

QY 61 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070
```

Db 1011 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1070
QY 121 GT 122
Db 1071 CT 1072

RESULT 20

US-10-641-643-1407
; Sequence 1407, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9441452
; SEQUENCE DESCRIPTION: SEQ ID NO: 1407 :
US-10-641-643-1407

Query Match 46.7%; Score 120.4; DB 7; Length 4164;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 970 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
QY 61 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 1030 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1089
QY 121 GT 122
Db 1090 CT 1091

RESULT 21

US-10-741-601-229
; Sequence 229, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229
; LENGTH: 4221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-229

Query Match 46.7%; Score 120.4; DB 7; Length 4221;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1009 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1068
QY 61 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 1069 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1128
QY 121 GT 122
Db 1129 CT 1130

RESULT 22

US-10-741-600-622
; Sequence 622, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622
; LENGTH: 4221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-622

Query Match 46.7%; Score 120.4; DB 8; Length 4221;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1009 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1068
QY 61 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
Db 1069 GGCTACCATGCCAGATGCCAGCATCAGAGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1128
QY 121 GT 122
Db 1129 CT 1130

RESULT 23

```
US-10-688-845-37
; Sequence 37, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
; APPLICANT: Lotze, Michael T
; APPLICANT: Tahara, Hideaki
; TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
; FILE REFERENCE: UPT-004
; CURRENT APPLICATION NUMBER: US/10/688,845
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,865
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 4150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-688-845-37

Query Match      46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 3.5e-27;
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 979 CAGCGGAGTGATGCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCACTATGCT 1038
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1039 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1098
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |
Qy 1099 CT 1100
Db |

RESULT 24
US-10-929-182-33
; Sequence 33, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; FILE REFERENCE: Multiple Sclerosis
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-33

Query Match      36.1%; Score 93.2; DB 9; Length 3444;
Best Local Similarity 85.2%; Pred. No. 3.6e-19;
Matches 104; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 736 CAGCGGAACGATGGGAAGCATGACTTCGGGATCTGGAATTCAGATCTCCAGCTCATCCGCTACGCT 795
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 796 GGCTACCAGATGCCCGATGGCACCATCAGAGGGGATCTGTCACCTTTGGAGTTCAACCCAG 855
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |
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Db 856 TT 857

RESULT 25
US-09-870-759-123
; Sequence 123, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-870-759-123

Query Match      35.5%; Score 91.6; DB 3; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTACGCT 1041
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1042 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTCAACCCAG 1101
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |
Qy 1102 TT 1103
Db |

RESULT 26
US-09-751-708A-123
; Sequence 123, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-751-708A-123

Query Match      35.5%; Score 91.6; DB 3; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGGAATTCACCTCAG 120
Db 1042 GGCTACCAAGATGCCCGGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101
Qy 121 GT 122
Db 1102 TT 1103

RESULT 27
US-10-428-817A-119
; Sequence 119, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(3690)
US-10-428-817A-119

Query Match 35.5%; Score 91.6; DB 8; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGGAATTCACCTCAG 120
Db 1042 GGCTACCAAGATGCCCGGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101
Qy 121 GT 122
Db 1102 TT 1103

RESULT 28
US-10-937-758A-100
; Sequence 100, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A

; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-10-937-758A-100

Query Match 35.5%; Score 91.6; DB 9; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGGAATTCACCTCAG 120
Db 1042 GGCTACCAAGATGCCCGGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101
Qy 121 GT 122
Db 1102 TT 1103

RESULT 29
US-10-182-049-18
; Sequence 18, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/182,049
; FILE REFERENCE: RTSP-0360
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 18
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(3690)
US-10-182-049-18

Query Match 35.5%; Score 91.6; DB 9; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041
Qy 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGGAATTCACCTCAG 120
Db 1042 GGCTACCAAGATGCCCGGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101
Qy 121 GT 122
Db 1102 TT 1103

RESULT 30
US-10-631-467-966
; Sequence 966, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631.467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 966
; LENGTH: 3991
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-631-467-966

Query Match 35.5%; Score 91.6; DB 9; Length 3991;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
|||||
Db 911 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTAGCT 970
|||||

Qy 61 GGCTACCAGATGCCAGATGCGCAGATCAGAGGGACCTGCCAACGTGGAATTCACCTCAG 120
|||||
Db 971 GGCTACCAGATGCCGATGGCCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030
|||||

Qy 121 GT 122
1031 TT 1032

RESULT 31
US-10-631-467-1064
; Sequence 1064, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631.467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1064
; LENGTH: 3991
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-631-467-1064

Query Match 35.5%; Score 91.6; DB 9; Length 3991;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
|||||
Db 911 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTAGCT 970
|||||

Qy 61 GGCTACCAGATGCCAGATGCGCAGATCAGAGGGACCTGCCAACGTGGAATTCACCTCAG 120
|||||
Db 971 GGCTACCAGATGCCGATGGCCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030
|||||

Qy 121 GT 122
1031 TT 1032

Db 971 GGCTACCAGATGCCGATGGCCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030
|||||

Qy 121 GT 122
1031 TT 1032

Db 1031 TT 1032

RESULT 32
US-10-305-720-1477
; Sequence 1477, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1477
; LENGTH: 4079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g951318
US-10-305-720-1477

Query Match 30.3%; Score 78.2; DB 6; Length 4079;
Best Local Similarity 77.2%; Pred. No. 1.8e-14;
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
|||||
Db 1412 CAGAGGACAGAGCGGCAAGCAGCACTTCCGAGTCTGGAACTCCCGAGCTCATCCGCTAGCT 1471
|||||

Qy 61 GGCTACCAGATGCCAGATGCGCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
|||||
Db 1472 GGCTACAAGCAGCGCTCAGCGCTCCACCCTGGGGGACCCAGCAATGTGCAGTTTCACAGAG 1531
|||||

Qy 121 GTA 123
1532 ATA 1534

Db 1532 ATA 1534

RESULT 33
US-10-475-049A-1
; Sequence 1, Application US/10475049A
; Publication No. US20050019854A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Rene
; APPLICANT: Lajoix, Anne-Dominique
; APPLICANT: Ribes, Gerard
; TITLE OF INVENTION: Novel Method For Screening Inhibitors of
; TITLE OF INVENTION: the Linkage Between the Neuronal Nitric Oxide Synthase
; TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal
; TITLE OF INVENTION: Nitric Oxide Synthase
; FILE REFERENCE: 50319/005001
; CURRENT APPLICATION NUMBER: US/10/475,049A
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/FR02/01327
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: FR 01/05248
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4290
; TYPE: DNA
; ORGANISM: Rattus rattus

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4287)
; OTHER INFORMATION:
; US-10-475-049A-1
;
; Query Match
; Best Local Similarity 29.3%; Score 75.6; DB 8; Length 4290;
; Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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QY 1 CAGCGAGTGATGGCAAGCAGACACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
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Db 1390 CAGAGGACTGACGGCAACATGACTTCCGAGTGTGGAATCAGCTCATCCGCTACGCG 1449
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QY 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
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QY 121 GT 122
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Db 1510 AT 1511
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; RESULT 34
; US-09-925-065A-56987
; Sequence 56987, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56987
; LENGTH: 700
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-56987
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; Query Match
; Best Local Similarity 22.3%; Score 57.6; DB 4; Length 700;
; Matches 81; Conservative 1; Mismatches 40; Indels 0; Gaps 0;
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Db 508 CAGCGCTGCCCTTGCGCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGCG 567
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QY 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
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Db 568 GGCTACCGGAGCAGGATGGCTCTGTGCGGGGGAGCCAGCCAACTGGAGATCACCAG 627
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QY 121 GT 122
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Db 628 GT 629
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; RESULT 35
; US-10-889-121-8
; Sequence 8, Application US/10889121
; Publication No. US20040253685A1
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; GENERAL INFORMATION:
; APPLICANT: Sessa, William C.
; TITLE OF INVENTION: eNOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
; FILE REFERENCE: 044574-5046-01
; CURRENT APPLICATION NUMBER: US/10/889,121
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 09/956,699
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: PCT/US00/09913
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/129,550
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-889-121-8
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; Query Match
; Best Local Similarity 21.2%; Score 54.8; DB 8; Length 3612;
; Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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Db 697 CAGCGCTGCCCTTGCGCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGCG 756
   |||||
QY 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
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Db 757 GGCTACCGGAGCAGGAGCGGCTCTGTGCGGGGGAGCCAGCCAACTGGAGATCACCAG 816
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QY 121 GT 122
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Db 817 CT 818
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; RESULT 36
; US-10-305-720-1234
; Sequence 1234, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1234
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 gi189259
; US-10-305-720-1234
;
; Query Match
; Best Local Similarity 21.2%; Score 54.8; DB 6; Length 3690;
; Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
;
QY 1 CAGCGAGTGATGGCAAGCAGACACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
   |||||
Db 717 CAGCGCTGCCCTTGCGCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGCG 776
   |||||
QY 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAACTGGAATTCACCTCAG 120
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Db 777 GGCTACCGGAGCAGGAGCGGCTCTGTGCGGGGGAGCCAGCCAACTGGAGATCACCAG 836
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QY 121 GT 122
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Db      837 CT 838

RESULT 37
US-10-305-720-1369
; Sequence 1369, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1369
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g434699
US-10-305-720-1369

Query Match      21.2%; Score 54.8; DB 6; Length 4035;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Db      748 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGGCTACGCG 807
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Qy      61 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAAATTCACCTCAG 120
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Db      808 GGCTACCGGAGCAGGAGCGCTCTGTGCGGGGGGACCAGCCAACTGGAGATCACCGAG 867
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Qy      121 GT 122
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Db      868 CT 869

RESULT 38
US-10-172-118-414
; Sequence 414, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 414
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M93718
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-414
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Query Match      21.2%; Score 54.8; DB 6; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy      61 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAAATTCACCTCAG 120
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Qy      121 GT 122
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Db      863 CT 864

RESULT 39
US-10-342-887-414
; Sequence 414, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 414
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-414

Query Match      21.2%; Score 54.8; DB 7; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Db      743 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGGCTACGCG 802
      |||||

Qy      61 GGCTACACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGAAATTCACCTCAG 120
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Qy      121 GT 122
      |
Db      863 CT 864

RESULT 40
US-10-889-121-9
; Sequence 9, Application US/10889121
; Publication No. US20040253685A1
; GENERAL INFORMATION:
; APPLICANT: Seesa, William C.
; TITLE OF INVENTION: eNOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
; FILE REFERENCE: 044574-5046-01
; CURRENT APPLICATION NUMBER: US/10/889,121
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Wed Dec 14 07:48:57 2005

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; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 09/956,699
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: PCT/US00/09913
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/129,550
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-889-121-9

Query Match      21.2%; Score 54.8; DB 8; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Db      ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
743 CAGCGTGCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGTGCGCTACGCG 802

QY      61 GGCTACCCAGATGCCAGATGCGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACTCAG 120
Db      ||||| | || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
803 GGCTACCCGAGCAGCAGCAGCGCTCTGTGCGGGGGGACCAGCCAACTGGAGATCACCGAG 862

QY      121 GT 122
Db      ||
863 CT 864
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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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405.271 Million cell updates/sec

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Searched: 3392430 seqs, 186927314 residues

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32.8	12.7	3001	7	US-11-145-703-194
2	32.2	12.5	2827	6	US-10-750-185-59391
3	31	12.0	154452	7	US-11-121-086-74
4	31	12.0	168516	7	US-11-121-086-3
5	30.6	11.9	2840	6	US-10-750-185-60778
6	30	11.6	4745	6	US-10-909-125-837
7	29.8	11.6	1678	6	US-10-750-185-43745
8	29.8	11.6	171162	7	US-11-112-908-38
9	29.4	11.4	1009	6	US-10-750-185-63750
10	29.4	11.4	1676	6	US-10-750-185-31860
11	29.4	11.4	3138	6	US-10-750-185-62600
12	29.4	11.4	179666	7	US-11-121-086-67
13	29.2	11.3	164810	7	US-11-121-086-4
14	29	11.2	3772	7	US-10-821-234-671
15	29	11.2	162289	7	US-11-121-086-20
16	28.8	11.2	600	6	US-10-750-185-868
17	28.8	11.2	1564	6	US-10-750-185-56551
18	28.6	11.1	861	6	US-10-750-185-54914
19	28.6	11.1	1196	6	US-10-750-185-34965
20	28.6	11.1	1543	6	US-10-750-185-25939
21	28.6	11.1	171486	7	US-11-121-086-105
22	28.4	11.0	2335	6	US-10-750-185-45463
23	28.4	11.0	172543	7	US-11-121-086-6

C 24	28.2	10.9	2333	6	US-10-645-441-6
C 25	28.2	10.9	2532	6	US-10-645-441-11
C 26	28.2	10.9	3745	6	US-10-750-185-26897
C 27	28.2	10.9	4226	6	US-10-750-185-61399
C 28	28	10.9	1215	6	US-10-750-185-56711
C 29	28	10.9	3132	6	US-10-392-234A-33
C 30	27.8	10.8	792	6	US-10-821-234-551
C 31	27.8	10.8	2233	6	US-10-750-185-44988
C 32	27.8	10.8	2498	6	US-10-131-826A-483
C 33	27.8	10.8	4305	7	US-11-080-991-67
C 34	27.8	10.8	163162	7	US-11-121-086-66
C 35	27.8	10.8	179892	7	US-11-112-908-39
C 36	27.6	10.7	2085	6	US-10-496-711-1
C 37	27.6	10.7	149419	7	US-11-112-908-49
C 38	27.6	10.7	161726	7	US-11-112-908-48
C 39	27.6	10.7	161726	7	US-11-112-908-52
C 40	27.6	10.7	163162	7	US-11-121-086-66
C 41	27.6	10.7	166111	7	US-11-112-908-47
C 42	27.4	10.6	600	6	US-10-750-185-20492
C 43	27.4	10.6	1934	6	US-10-750-185-32804
C 44	27.4	10.6	2236	6	US-10-131-826A-381
C 45	27.4	10.6	126552	7	US-11-121-086-1

ALIGNMENTS

RESULT 1
US-11-145-703-194
; Sequence 194, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bouguetere, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53 US16 DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 194
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-26223-225 : polymorphic base G or T

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Sequence 11, Appli
Sequence 26897, A
Sequence 61399, A
Sequence 56711, A
Sequence 33, Appli
Sequence 551, App
Sequence 44988, A
Sequence 67, Appli
Sequence 66, Appli
Sequence 39, Appli
Sequence 1, Appli
Sequence 49, Appli
Sequence 48, Appli
Sequence 52, Appli
Sequence 66, Appli
Sequence 47, Appli
Sequence 20492, A
Sequence 32804, A
Sequence 381, App
Sequence 1, Appli


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; NAME/KEY: misc_binding
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-26223-225.mis1,
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1502..1520
; OTHER INFORMATION: 99-26223-225.mis2, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1277..1297
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1842..1862
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-26223-225 probe
; US-11-145-703-194

Query Match      12.7%; Score 32.8; DB 7; Length 3001;
Best Local Similarity 51.4%; Pred. No. 1.7;
Matches 76; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy      62 GCTACCGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACTCAGG 121
Db      862 GCAAGAAGATGCAAAATTTACTCTTAACCTTTGAAACCATATAAAACATTTCCAGGCCAATCAAG 921

Qy      122 TACCGCGCCAGCTCAGCRRCCGCGCATTTGGGGGGGAGCCCGTGTGAGCGACTGA 181
Db      922 AACACTTCCCTGCTCTACTTCCAGAGACAGAAGAGAGACAGAGAGAGAGGTGAGAGA 981

Qy      182 CAGAGTGGAGCCCGCAGAGGAGACAGCGCAG 209
Db      982 CAGAATGTGAGGAGAGAGAAACATGTAG 1009

RESULT 2
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; Sequence 59391, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59391
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Bovine 19866880650684
; US-10-750-185-59391

Query Match      12.5%; Score 32.2; DB 6; Length 2827;
Best Local Similarity 46.3%; Pred. No. 2.4;
Matches 106; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy      22 GACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGTGCTACCCAGATGCCAGATGGC 81
Db      1014 GAATTCCTGCTGGGCAAGGCCATGGCCCTCATCTTTGTGGGCGCGGTGCCCCAGGGTGGC 1073

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Qy      82 AGCATCAGAGGGGACCTCCACAGCTGGAATTCACCTAGTACCGCGGCCAGCCTCAGCC 141
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Qy      142 RCCGGCCATTGGGGCGGGAGCCCCGTGGTGACGAGTGACAGAGTGGAGCCCGCAGAGGAG 201
Db      1134 TGTGGCTGTGCACACAGGCTGTGTCCTCAAGTGTGAGGCTGAGAGAGCTACAGCCGGATGAG 1193

Qy      202 ACACGAGCCCGGGTTTACAGACTCACAGGGCCCGTCTTGTTCCTCCAGC 250
Db      1194 GCAGGCATGACAGCAAGGTGCTGGACACCGCCCATGTCAGGCGCTTCATC 1242

RESULT 3
US-11-121-086-74
; Sequence 74, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74
; LENGTH: 154452
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-74

Query Match      12.0%; Score 31; DB 7; Length 154452;
Best Local Similarity 58.4%; Pred. No. 7.7;
Matches 52; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

Qy      127 GCGCCAGCCTCAGCCRCGCGCCATTGGGGCGGGAGCCCGTGTGAGCGCAGTACAGAG 186
Db      117867 GCGCCTGGCGCTGCCGATGCCCTCGGGGTTCGAGCGCGACGCGGGCGAGCCGCGCGCGGC 117926

Qy      187 TCGAGCCCGCAGAGACAGACGACGCGCCCGG 215
Db      117927 TCCAGCGCGCGCGGAGAGACGCGGAGG 117955

RESULT 4
US-11-121-086-3
; Sequence 3, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 168516
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-3

Query Match      12.0%; Score 31; DB 7; Length 168516;
Best Local Similarity 56.7%; Pred. No. 7.7;
Matches 55; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

Qy      121 GTACCCGCGCCAGCCTCAGCCRCGCGCCATTGGGGCGGGAGCCCGTGTGAGCGAGTG 180

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Db 98271 GTTCTGCGCGGACGACGACGACGAGGCGGGTGGGGCTTGGTCAGCACGTG 98330
QY 181 ACAGATGGAGCCAGAGGAGACACGAGCCCGGGCT 217
Db 98331 GCAGGGGTGTGGCCACGCGCAGAGGACACCTGACGCT 98367

RESULT 5
US-10-750-185-60778/c
; Sequence 60778, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 60778
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Bovine 19866880571363
US-10-750-185-60778

Query Match 11.9%; Score 30.6; DB 6; Length 2840;
Best Local Similarity 60.8%; Pred. No. 6.8;
Matches 48; Conservative 1; Mismatches 30; Indels 0; Gaps 0;
QY 121 GTACCGCGCCAGCCTGACGCGCCATTTGGCGGGGAGCCCGTGTGAGCGAGTG 180
Db 2355 GCATCTCTCCCGCGCCAGCTGACGCGCTCTGGGGATGATACCCCGTGTCCATCTGTG 2296

QY 181 ACAGATGGAGCCAGAGG 199
Db 2295 ACAGATGGAGCCCGAGG 2277

RESULT 6
US-10-909-125-837/c
; Sequence 837, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303

; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 837
; LENGTH: 4745
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-909-125-837

Query Match 11.6%; Score 30; DB 6; Length 4745;
Best Local Similarity 52.5%; Pred. No. 10;
Matches 63; Conservative 1; Mismatches 56; Indels 0; Gaps 0;
QY 53 GCTATGCTGGCTACCGATGCCAGATGCCAGATGCAGAGGAGCCCTGCCACGTTGGAT 112
Db 756 GCGCGATGGCTGCGAGCAGCGCGCGCTCCCGAGCGGGCGCAGCCACGCGCGG 697
QY 113 TCACCTCAGGTACCGCGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGAGCCCGTGGTG 172
Db 696 CCGCGCGCGCACCGTTCCTCCGCGGGCGGACGCGCGGGGACCCCGCGCGG 637

RESULT 7
US-10-750-185-43745
; Sequence 43745, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 43745
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Bovine 19866880599390
US-10-750-185-43745

Query Match 11.6%; Score 29.8; DB 6; Length 1678;
Best Local Similarity 55.2%; Pred. No. 11;
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 66 CCAGATGCCAGATGCCAGATGCAGAGGAGCCCTGCCACGTTGGATTCACCTCAGGTACC 125
Db 692 CCATGTTCCAGTAAGCCTATTACATGAGACCTGTCTTCTCTGGACTTGACTTCTACT 751
QY 126 CGGCCCGAGCCTCAGCCRCGCGCATTTGGGGCGGGAGCCCGGTGG 170
Db 752 CGGCCCGAGCCTCAGGCAAGGCTGTCTGGAGATCAGTCCAGTGG 796

RESULT 8
US-11-112-908-38/c
; Sequence 38, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers

```
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

Query Match      11.6%; Score 29.8; DB 7; Length 171162;
Best Local Similarity 48.0%; Pred. No. 17;
Matches 82; Conservative 1; Mismatches 88; Indels 0; Gaps 0;

Qy 46 CTCATCCGCTATGCTGCTACAGATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAAC 105
Db 12535 CCCACACCCCGCGCGCGCGCTCCACCTGCTCCACCCCGCGGGGCGCGCGCC 12476

Qy 106 GTGGAATTCATCAGGTACCGCGCCAGCCCTCAGCCRCGCCCATTTGGGGCGGGAGCCCC 165
Db 12475 CGGCCCGCGCGCTGGCACCGCGCGCGCGCTGGGGCGGAGCGAGCGCGCGG 12416

Qy 166 CGTGTGAGCGAGTGTGAGTGGAGCCCGAGAGAGACAGCCAGCCCGCGG 216
Db 12415 GCGAGAGGGCGAGCGCCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGC 12365

RESULT 9
US-10-750-185-63750/c
; Sequence 63750, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63750
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Bovine 19866880851319
US-10-750-185-63750

Query Match      11.4%; Score 29.4; DB 6; Length 1009;
Best Local Similarity 49.0%; Pred. No. 13;
Matches 75; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

Qy 98 CTGCCAAGCTGAATTCATCAGGTACCGCGCCAGCCCTCAGCCRCGCCCATTTGGGGCG 157
Db 782 CTGCCACCTCCGCGGTTGGGTGGGACCCGCTGGGCTGTAGGGGCAACTCAGAGGGCT 723

Qy 158 GGGAGCCCGGTGGTGGAGGAGTGACAGAGTGGAGCCAGAGAGAGACAGCAGCCCGGGCT 217
Db 722 CTGAGCCAGAGAGGGTGGGCCCAAGATTCCACTTAAACAATCTGGGGGTCTCTTAT 663
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Qy 218 TACAGACTCAGAGCGCCGCTCTTGTTCGCCAGC 250
Db 662 TCCTGTAACGAGGGCGGCCCTAGGTCCCCCAGC 630

RESULT 10
US-10-750-185-31860/c
; Sequence 31860, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31860
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Bovine 19866881075748
US-10-750-185-31860

Query Match      11.4%; Score 29.4; DB 6; Length 1676;
Best Local Similarity 52.9%; Pred. No. 14;
Matches 63; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 64 TACCAGATGCCAGATGCCAGATCAGAGGGGAGCCCTGCCAACCTGGAATTCATTCAGGTA 123
Db 629 TACCAGAGACCTTATGCCAGGTGCTTCTGTGAGTGCAGATGCACACTGCTG 570

Qy 124 CCGCGCCAGCCTCAGCCRCGCCCATTTGGGGCGGGAGCCCGTGGTGTGAGCGAGTGAC 182
Db 569 CACAGCCTCCGCTGTGCCAGAGCCAGTGTACTGTGAGAGCTGTGATGGTCTTGAGAC 511

RESULT 11
US-10-750-185-62600/c
; Sequence 62600, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62600
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Bovine 19866881144324
US-10-750-185-62600

Query Match      11.4%; Score 29.4; DB 6; Length 3138;
Best Local Similarity 55.7%; Pred. No. 15;
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```
Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
QY 53 GCTATCTGCTACCATGCGCCAGATGCGAGCATCAGAGGGACCTGCCAAGTGGAT 112
DB 1370 GCTACACCTCTCCAGCTGCCATTTTTCGAAGTGCAGAAACTGCCCACTGAGGCAG 1311
QY 113 TCACCTAGGTACCGCGCCAGCCCTCAGCCRCGCGCCA 149
DB 1310 CAGAAGCAACACCCAGCAGAGCTCAGCCCAATGCACA 1274

RESULT 12
US-11-121-086-67/c
; Sequence 67, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 179666
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-67

Query Match 11.4%; Score 29.4; DB 7; Length 179666;
Best Local Similarity 54.3%; Pred. No. 22; Indels 0; Gaps 0;
Matches 57; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

QY 135 CTCAGCCRCGCGCATTTGGGGCGGAGCCCGTGTGAGCGAGTGACAGATGGAGCCC 194
DB 163368 CACACCGGGCGGGAGTGGAAACGGGAGCCAGATCGGAGCCAGCATGGAGCGGCAC 165309
QY 195 AGAGGAGACGACGACCGCGGCTTACAGACTCACAGGCGCGTCT 239
DB 165308 AGACGAGCGATAGAGCGCTGGGTGGAGCGGCGGCGTCTCAGCT 165264

RESULT 13
US-11-121-086-4
; Sequence 4, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 164810
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-4

Query Match 11.3%; Score 29.2; DB 7; Length 164810;
Best Local Similarity 57.8%; Pred. No. 24; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 156 CGGGGAGCCCGTGTGAGCGAGTGACAGAGTGGAGCCCGCAGAGAGACACGACGCCGGG 215
DB 131807 CGGGGAGCCCGTGTGAGGAGAGGGGCCACTGCTGAGGCTGGAGCGAGGAGGAGG 131866
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QY 216 CTTACAGACTCACAGGCGCGCTGTGTGTTCC 245
DB 131867 CTGACTGCTCTCTGGGCTTAGTTTCTCC 131896

RESULT 14
US-10-821-234-671
; Sequence 671, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suean
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 671
; LENGTH: 3772
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-671

Query Match 11.2%; Score 29; DB 6; Length 3772;
Best Local Similarity 49.7%; Pred. No. 19; Indels 0; Gaps 0;
Matches 71; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY 93 GCAGCCTGCCAACGTGGAATTCACCTCAGGTACCGGCCCGCAGCTCAGCCRCGCGCATTTG 152
DB 1545 GGAGCTGGCTGTCTTGGCATCCGCCAGAGCTGTCTGCTGTGAGCCCGGCTGT 1604
QY 153 GGGCGGGAGCCCGCTGGTGTGAGCGAGTGACAGAGTGGAGCCCGCAGAGGAGACACGACGCC 212
DB 1605 GGGCGCTCCCGGGTGTGAGCGGAGAGGAGCGAGGCGAGGCGAGGCGACTTCAGCCCT 1664
QY 213 GGGCTTACAGACTCACAGGCGCC 235
DB 1665 GTGCCTGGAGCCTGCAGGCTCTC 1687

RESULT 15
US-11-121-086-20/c
; Sequence 20, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 162289
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-20

Query Match 11.2%; Score 29; DB 7; Length 162289;
Best Local Similarity 50.4%; Pred. No. 27; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 46 CTCATCCGCTATCTGCTTACCATGCGCAGATGGCAGATGGCAGGAGCCCTGCCAAC 105
```

Db	108108	CTCAGCCCCCTACCTGTGGCAGCCTGTTGGCCCTGTGCCCCCTCAGTGGAGAGACGGAGGTCAAT	108049
Qy	106	GTGGAAATTCACACAGTACCCGGGCCAGCCTCAGCCRCCTGGCCATTTGGGGCGGGAGCCC	165
Db	108048	GGCAGGTTTCACGAAGCAGAGCTTATCCACAGGCAAAACGACACACACAGAGCTGTCTCTGGGCA	107989
Qy	166	CGTGGTGAGCGAGTGACAGAG	186
Db	107988	CGTGGTGAGCACATGACAGAG	107968

```

RESULT 16
US-10-750-185-868/c
; Sequence 868, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 868
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-868

```

		Query Match	11.2%	Score 28.8;	DB 6;	Length 600;	
		Best Local Similarity	56.7%;	Pred. No. 18;			
		Matches	51;	Conservative	1;	Mismatches	38; Indels 0; Gaps 0;
Qy	79	GCGAGCATCAGAGGGGACCTTGCACAAGTGGAATTCACTACGTACC					
Dd	359	GGTATGCTGAGCTGGGACCGAGGACACTGATTCTGGACAGGGTCCTCTCAGG					
Qy	139	GCCRCGGGCCATTGGGGGGGGAGCCCCCGT					
Dd	299	GCCACCTCTCATTGGGGCAGCCCCCTCCT					

```

RESULT 17
US-10-750-185-56551/c
; Sequence 56551, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR I
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,48
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 56551
; LENGTH: 1564
; TYPE: DNA

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; ORGANISM: Bovine
US-10-750-185-56551

Query Match      11.2%; Score 28.8; DB 6; Length 1564;
Best Local Similarity 54.8%; Pred. No. 20;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 155 GCGGGAGCCCCGTGGTGACCGAGTACACAGTGGAGGCCAGAGGAGACACGAGACCCGG 214
      |||||
Db 1394 GCGGGTGGCCCTGGTGGCTGAGGGTAAGGGGATGGATGACCTGAGGGGGCTTCAGAGTGG 1335

Qy 215 GCTTACAGACTACAGGGCCCGTCTGTTCCTCCAGCTGTGCATC 258

Db 1334 GCTGAGGGCCCTGAAGGGGACATCTTGTCTTACCTGAGGTTCCCTC 1291

```

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RESULT 18
US-10-750-185-54914
; Sequence 54914, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54914
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-54914

```

	Query Match	Best Local Similarity	Score	DB 5	Length	861;
	Matches	Conservative	55.6;	Pred. No. 22;	Mismatches	Indels
			0;		0;	Gaps
Qy	82	AGCATCAGAGGGGACCTGCGAACGTCGGAA	TTC	ACTCAGGTACCCGGGCCAGCCTCAGCC	141	
Db	408	AGCAGCCGAGGCGCTGGGACCTGCGCGGGACTG	CTCTAGGGCCGGGCGCTGCCCCAGCC	467		
Qy	142	RCGCGCCATTGGGCGGGGAGCCCGCTGGTGAGCGAGTG	180			
Db	468	CGGGGCCAGCAGCAGACAGCCAGCCTCGTGGGGCGCG	506			

```

RESULT 19
US-10-750-185-34965/c
? Sequence 34965, Application US/10750185
? Publication No. US20050260603A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: FANTIN, Dennis
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM1100-2
? CURRENT APPLICATION NUMBER: US/10/750,185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31

```

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34965
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Bovine 19866880885427
US-10-750-185-34965

Query Match 11.1%; Score 28.6; DB 6; Length 1196;
Best Local Similarity 53.2%; Pred. No. 23;
Matches 58; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 128 GCCACGCTCAGCCRCGCCCAATTGGGGGGGGAGCCCGTGTGAGCGAGTGACAGACT 187
DB 386 GCCACGCTCACACGTCACCTTCTGGGGGGGTGGGAGGGGCTGGGGGACAAATG 327
QY 188 GGAGCCCAAGGAGACACGAGCCCGGCTTACAGACTCACAGGGCCCG 236
DB 326 GGGGGGAAGCAGGCAGATGGAGGGTGGGGGCCACAGGCACAGTAAACG 278

RESULT 20

US-10-750-185-25939/c
; Sequence 25939, Application US/10750185
; Publication No. US20050260603A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25939
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Bovine 19866880394315
US-10-750-185-25939

Query Match 11.1%; Score 28.6; DB 6; Length 1543;
Best Local Similarity 53.2%; Pred. No. 23;
Matches 58; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 108 GGAATTCACCTCAGGTACCCGGCCAGCTCAGCCRCGGCCATTGGGGGGGGAGCCCG 167
DB 843 GGGACCGACTGAGGACCTGCACCCGGTTCCGGAGCCATCCAGGCTGGGGGTGAGCTGG 784
QY 168 TGTGTGCGAGTGCACAGATGAGAGCCCGCAGAGGACACGAGCCCGGGC 216
DB 783 GGATGGGTGCTCAGTGGGAGGAGCGGCTGAAGATGGCAGGCGCTGGGC 735

RESULT 21

US-11-121-086-105
; Sequence 105, Application US/11121086
; Publication No. US20050266459A1

GENERAL INFORMATION:

; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

Query Match 11.1%; Score 28.6; DB 7; Length 171486;
Best Local Similarity 50.8%; Pred. No. 36;
Matches 90; Conservative 1; Mismatches 85; Indels 1; Gaps 1;

QY 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTAG 120
DB 97825 GCGGGGAGAGGCTTTCAGAGCTGACTCTCTTGGGTGAAACGCGACTTGGAGGGACGCCG 97884
QY 121 GTACCCGGCCAGCTCAGCCRCGGCCA-TTGGGGGGGGAGCCCCGTGGTGAGCGACT 179
DB 97885 CAGCCGAGACGTTTCAGCTCCGGGCGACGACTTCGGGCTGGGGACGGCGTGGCGT 97944
QY 180 GACAGATGGAGCCCGCAGGAGACACGAGCCCGGCTTACAGACTCACAGGGCCCG 236
DB 97945 GGCAGGGTGTCCCGAGAGGAAGCCGCCACCGGAGGCGCCGCCCTTGGCCCG 98001

RESULT 22

US-10-750-185-45463
; Sequence 45463, Application US/10750185
; Publication No. US20050260603A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45463
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Bovine 19866880456049
US-10-750-185-45463

Query Match 11.0%; Score 28.4; DB 6; Length 2335;
Best Local Similarity 48.2%; Pred. No. 27;
Matches 80; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGGCAAGCAGCAGCTTCGGGTGTGAATGTCACTCAGCTCATCCCGTATGCT 60
DB 215 CTGCAGGGCAATGCCTTGCCAGGAAACGAGGCCCCCAAGCCCTTCAACCA 274
QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCATCTAG 120
DB 275 CAACAGCAGAGCCAGCGGAGGGCTCAGAGGGGTCTTCCCTCCCGAGTAAAGTCAGAAGC 334
QY 121 GTACCCGGCCAGCTCAGCCRCGGCCATTGGGGGGGGAGCCCC 166
DB 335 GAGGACAGAAGACCCCGGACCTGGGACCTGGAGCGAGGGGGCCACC 380

RESULT 23

US-11-121-086-6/c
; Sequence 6, Application US/11121086
; Publication No. US20050266459A1

GENERAL INFORMATION:

```
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 172543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-6

Query Match 11.0%; Score 28.4; DB 7; Length 172543;
Best Local Similarity 66.1%; Pred. No. 40;
Matches 41; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 174 GCGAGTACACAGTGGAGGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCACAGGC 233
Db 115469 GCGTGGGAGGAGCGGGCCCGAGCTGCGGTGCTGCGCGGGTACAGACTCTCTGGC 115410

Qy 234 CC 235
Db 115409 CC 115408

RESULT 24
US-10-645-441-6/c
; Sequence 6, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse T1R2 sweet taste receptor
US-10-645-441-6

Query Match 10.9%; Score 28.2; DB 6; Length 2332;
Best Local Similarity 45.5%; Pred. No. 31;
Matches 96; Conservative 1; Mismatches 114; Indels 0; Gaps 0;

Qy 38 ATGCTCAGCTCATCCGCTATGCTGCTATCCAGATGCCAGATGCCAGATGCCAGGGGACC 97
Db 2087 AGGCCACCTTGACGGCGGTGATGAAGGCCACGAAGACGTAGGGCCGTGGTAACGCATC 2028

Qy 98 CTGCCAACGTGGAAATTCACCTCAGGTACCCGGCCCGAGCCTCAGCCRCGGCCCATTTGGGCG 157
Db 2027 CAGAAACCGTAGGCGCTTGGCAGGCGCTGCGCCATCTTGAAGACGACACAACTTGAAG 1968

Qy 158 GGGAGCCCGTGTGACCGAGTGCAGAGTGGAGCCCGAGAGGAGACACGAGCCCGGCT 217
Db 1967 GAGCGACCGTGTGATGACGAGGAGGAGCAGACCGGAGCAAGCAAAAGCTTGAAGCTTGGCG 1908

Qy 218 TACAGACTCACAGGCCCGCTTGTTCCTCCCA 248
Db 1907 CAGAAACAGGAGAACCGTGGGGGGGCCCA 1877

RESULT 26
US-10-185-26897/c
; Sequence 26897, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
```

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Qy 158 GGGAGCCCGTGTGACCGAGTGCAGAGTGGAGCCCGAGAGGAGACACGAGCCCGGCT 217
Db 1765 GAGGAACTGTGACGACGAGGAGAGATGTTGTAACCAAGGGCAAGAGGGCTTGGCT 1706

Qy 218 TACAGACTCACAGGCCCGCTTGTTCCTCCCA 248
Db 1705 AGCAAGCAGCAGAGCCCTTGTGGTTCCCA 1675

RESULT 25
US-10-645-441-11/c
; Sequence 11, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2532
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse T1R2 sweet taste receptor
US-10-645-441-11

Query Match 10.9%; Score 28.2; DB 6; Length 2532;
Best Local Similarity 45.5%; Pred. No. 31;
Matches 96; Conservative 1; Mismatches 114; Indels 0; Gaps 0;

Qy 38 ATGCTCAGCTCATCCGCTATGCTGCTATCCAGATGCCAGATGCCAGATGCCAGGGGACC 97
Db 2087 AGGCCACCTTGACGGCGGTGATGAAGGCCACGAAGACGTAGGGCCGTGGTAACGCATC 2028

Qy 98 CTGCCAACGTGGAAATTCACCTCAGGTACCCGGCCCGAGCCTCAGCCRCGGCCCATTTGGGCG 157
Db 2027 CAGAAACCGTAGGCGCTTGGCAGGCGCTGCGCCATCTTGAAGACGACACAACTTGAAG 1968

Qy 158 GGGAGCCCGTGTGACCGAGTGCAGAGTGGAGCCCGAGAGGAGACACGAGCCCGGCT 217
Db 1967 GAGCGACCGTGTGATGACGAGGAGGAGCAGACCGGAGCAAGCAAAAGCTTGAAGCTTGGCG 1908

Qy 218 TACAGACTCACAGGCCCGCTTGTTCCTCCCA 248
Db 1907 CAGAAACAGGAGAACCGTGGGGGGGCCCA 1877

RESULT 26
US-10-185-26897/c
; Sequence 26897, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
```


Db 303 CCTGCCCGGCTGAGCTGCAGAACCGCTGAAGAAAGCCGAGGCGCATGCGCAGGC 362
Qy 201 GACAGGAGCCGGCTTACAGACTACAGAGCCCGCTTTCTTCCCGAGCTG 252
Db 363 GGTGCTGACCCAGGCGCTGCAGGTGCGAGACACGAGCGCGGTTCTCTGCTG 414

RESULT 30
US-10-821-234-551
; Sequence 551, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 551
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-551

Query Match 10.8%; Score 27.8; DB 6; Length 792;
Best Local Similarity 54.6%; Pred. No. 36;
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 140 CCRCCGGCCATTGGGGGGGAGCCCGCTGTGAGCGAGTGCAGAGTGGAGGCCAGAGG 199
Db 77 CCATGGGCTCGGGGAACCCGCGCGTGTGTTTGTGCTCCAGCGCCAGGAGG 136

Qy 200 AGACAGCGAGCCCGGGCTTACAGACTACAGGGCCCG 236
Db 137 CCACCTGCAGCGCTGTGCTCCAGACTGATGTCACCCG 173

RESULT 31
US-10-750-185-44988/c
; Sequence 44988, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 44988
; LENGTH: 2233
; TYPE: DNA
; ORGANISM: Bovine 19866880984581
US-10-750-185-44988

Query Match 10.8%; Score 27.8; DB 6; Length 2233;
Best Local Similarity 49.6%; Pred. No. 40;
Matches 68; Conservative 1; Mismatches 68; Indels 0; Gaps 0;

Qy 20 ACGACTTCCGGTGTGGAATCTCAGCTCATCGCTATGCTGCTACCCAGATGCCAGATG 79
Db 1440 ATGAGTACAGGTACCTTAAGTTCTTGGGCTTCCCGATGGCTCAGCAGGTAAAGAATCTG 1381
Qy 80 GCAGCATCAGAGGGACCCCTGCCAACGTGGAATTCATCAGGTACCCGCGCCAGCCTCAG 139
Db 1380 CCTGCAGTGCAGGAGATCCAGACAAATGGGTTTGACCCCTCGGTCGGGAAGAGCCCCCTG 1321

Qy 140 CCRCCGGCCATTGGGGC 156
Db 1320 GAGGAGGCCATTGTGAC 1304

RESULT 32
US-10-131-826A-483
; Sequence 483, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 483
; LENGTH: 2498
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-483

Query Match 10.8%; Score 27.8; DB 6; Length 2498;
Best Local Similarity 54.6%; Pred. No. 40;
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 140 CCRCCGGCCATTGGGGGGGAGCCCGCTGTGAGCGAGTGCAGAGTGGAGGCCAGAGG 199

Db 93 CCATGGGCTGGGGAAACCCCGCCCGTGGTGTGTTGCTGCCAGCAGGGCCAGGAG 152
QY 200 AGACAGCAGCCCGGGCTTACAGACTCACAGGCCCCG 236
Db 153 CCACCTGCAGCCTGGTGTCTCCAGACTGATGTACACCCG 189

RESULT 33
US-11-080-991-67
; Sequence 67, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Pether Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCES: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 4305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-67

Query Match 10.8%; Score 27.8; DB 7; Length 4305;
Best Local Similarity 50.4%; Pred. No. 42;
Matches 65; Conservative 1; Mismatches 53; Indels 0; Gaps 0;
QY 79 GGCAGCATCAGAGGGACCTGCGCAAGCTGTGGAATTCTCAGGTACCCGCCCGAGCTCA 138
Db 687 GTCATCACCAGCTGCACCCCGGCCACGCGCTCTCTCTGAGGGCGTGCAGCGCTCGCC 746
QY 139 GCRCCGGCCATGGGGCGGGAGCCCGTGTGAGGAGTGACAGAGTGGAGCCAGAG 198
Db 747 GAGCGCCAGCCAGCTGAGTTGGCGGCTGCTGAGCTGCTGAGCTGAGCTGGAGCTGGGCGCGGA 806
QY 199 GAGACAGCC 207
Db 807 GGGCCGCGC 815

RESULT 34
US-11-121-086-66
; Sequence 66, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCES: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 163162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-66

Query Match 10.8%; Score 27.8; DB 7; Length 163162;
Best Local Similarity 62.0%; Pred. No. 59;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 67 CAGATGCCAGTGCAGCATCAGAGGGGACCTGCGCAACGTGGAAATTCACCTCAGGTACCC 126

Db 32805 CAGAGGCTGTATCTGTATGATGGGACGCTGCCGACCAACTGTCTTCTGTGGCTCCC 32864
QY 127 GCCCAGCCTC 137
Db 32865 AGCAGCAGCCTC 32875

RESULT 35
US-11-112-908-39/c
; Sequence 39, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Lisa M.
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCES: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 179892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-39

Query Match 10.8%; Score 27.8; DB 7; Length 179892;
Best Local Similarity 54.6%; Pred. No. 59;
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;
QY 122 TACCCGGCCAGCCTCAGCCCGCCATTTGGGGCGGAGCCCGTGGTGAGCGAGTGA 181
Db 155215 TGCCCCACCCCTGCCACAGCCAGATGCCACTGACCATCAGGAGCGGGGGGTGTGAGCCA 155156
QY 182 CAGAGTGGAGCCCGAGAGGAGACAGCAGCGCCGGCTT 218
Db 155155 GGGGGTGCAGGGCTGGCGGGTGAAGCTGGCTGGGGTT 155119

RESULT 36
US-10-496-711-1/c
; Sequence 1, Application US/10496711
; Publication No. US20050256649A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: HIGH THROUGHPUT CORRELATION OF
; TITLE OF INVENTION: POLYMORPHIC FORMS WITH MULTIPLE PHENOTYPES WITHIN CLINICAL
; TITLE OF INVENTION: POPULATIONS
; FILE REFERENCES: PU4699WO
; CURRENT APPLICATION NUMBER: US/10/496,711
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: 60/344892
; PRIOR FILING DATE: 2002-12-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-496-711-1

Query Match 10.7%; Score 27.6; DB 6; Length 2085;
Best Local Similarity 56.7%; Pred. No. 45;
Matches 51; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 126 CGGCCAGCCTCAGCCRCGCGCCATTGGGCGGGAGCCCGTGTGTGAGCGAGTGACAGA 185
|||||
Db 1572 CGGCCCGGCCCGCTCCAGGATCTCGGGGCCGAGCTCCGCGTTCGCGCCCGGACTGT 1513
|||||
Qy 186 GTGGAGCCAGAGGAGACACGACGCCCGGG 215
|||||
Db 1512 CTCTCGGCTCTCGGCCCGCGCGCTCTGGG 1483
|||||

RESULT 37

US-11-112-908-49/c
; Sequence 49, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 149419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-49

Query Match 10.7%; Score 27.6; DB 7; Length 149419;
Best Local Similarity 45.9%; Pred. No. 66;
Matches 90; Conservative 1; Mismatches 105; Indels 0; Gaps 0;
Qy 16 AAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGGTACAGATGCCA 75
|||||
Db 48272 AAGCAACGCCCGGGGACCGGCTGCTGTGGGGCCACGCAAGCCAGAACCGAT 48213
|||||
Qy 76 GATGGCAGCATCAGAGGGACCTGCCAAGCTGGAATTCATCAGGTACCGCGCCAGCC 135
|||||
Db 48212 GCGCGTCCCTCGTGGGGCCGAGTTCAAAGAGCCGCGACCCCGACGCGCCCTTGC 48153
|||||
Qy 136 TCAGCCRCGCGCCATTGGGCGGGAGCCCGTGTGAGCGAGTGACAGAGTGAGGCCA 195
|||||
Db 48152 GAAGCCGGCGCCCTTCCCTCCGAGAGCAGGAGGGCGCCGCGGAGGGTGGCTCG 48093
|||||
Qy 196 GAGGAGACACGACGCC 211
|||||
Db 48092 GTGGAGCTGGCGCC 48077
|||||

RESULT 38

US-11-112-908-48/c
; Sequence 48, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 161726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-48

Query Match 10.7%; Score 27.6; DB 7; Length 161726;
Best Local Similarity 45.9%; Pred. No. 67;
Matches 90; Conservative 1; Mismatches 105; Indels 0; Gaps 0;
Qy 16 AAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGGTACAGATGCCA 75
|||||
Db 98554 AAGCAACGCCCGGGGACCGGCTGCTGTGGGGCCACGCAAGCCAGAACCGAT 98495
|||||
Qy 76 GATGGCAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCAGGTACCGCGCCAGCC 135
|||||
Db 98494 GCGCGTCCCTCGTGGGGCCGAGTTCAAAGAGCCGCGACCCCGCGCCCTTGC 98435
|||||
Qy 136 TCAGCCRCGCGCCATTGGGCGGGAGCCCGTGTGAGCGAGTGACAGAGTGAGGCCA 195
|||||
Db 98434 GAAGCCGGCGCCCTTCCCTCCGAGAGCAGGAGGGCGCCACGACGAGGGTGGCTCG 98375
|||||
Qy 196 GAGGAGACACGACGCC 211
|||||
Db 98374 GTGGAGCTGGCGCC 98359
|||||

RESULT 39

US-11-112-908-52/c
; Sequence 52, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 161726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-52

Query Match 10.7%; Score 27.6; DB 7; Length 161726;
Best Local Similarity 45.9%; Pred. No. 67;
Matches 90; Conservative 1; Mismatches 105; Indels 0; Gaps 0;
Qy 16 AAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGGTACAGATGCCA 75
|||||
Db 98554 AAGCAACGCCCGGGGACCGGCTGCTGTGGGGCCACGCAAGCCAGAACCGAT 98495
|||||
Qy 76 GATGGCAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCAGGTACCGCGCCAGCC 135
|||||
Db 98494 GCGCGTCCCTCGTGGGGCCGAGTTCAAAGAGCCGCGACCCCGCGCCCTTGC 98435
|||||
Qy 136 TCAGCCRCGCGCCATTGGGCGGGAGCCCGTGTGAGCGAGTGACAGAGTGAGGCCA 195
|||||

Db 98434 GAAGCGGCGGCTTCCCTCCAGAGGACACGAGGGCGCCACGACGAGGGTGGCTCG 98375
QY 196 GAGGAGACAGCGAGCC 211
Db 98374 GTGAGCCTGGGCGCC 98359

RESULT 40
US-11-121-086-66/c
; Sequence 66, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 163162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-66

Query Match 10.7%; Score 27.6; DB 7; Length 163162;
Best Local Similarity 51.6%; Pred. No. 67;
Matches 63; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 95 ACCCTGCCAACGTGGAATTACTCAGGTACCCGGCCCGCCTCAGCCRCGCGCCATTGGG 154
Db 52052 ACCGCGCATAAAGTTGGGGGCTCCCGAGCGCGCTCCCGAGCCGCCCTCACCTCGG 51993
QY 155 GCGGGGAGCCCGTGTGCGAGTGACAGAGTGGAGCCCGCAGAGGAGACAGCGCCCGG 214
Db 51992 CCGCGTGTCTCATGTCTAGCCCCCGCCCGCCCGCTCCACAGGCGCGCCCGG 51933
QY 215 GC 216
Db 51932 CC 51931

Search completed: December 13, 2005, 18:31:57
Job time : 249 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:21:57 ; Search time 660 seconds
(without alignments)
300.705 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatgcacagctgggggaacaagacg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	100.0	24	9	US-10-713-137-3
2	16.8	70.0	25	10	US-11-036-317-523844
3	15.8	65.8	25	7	US-10-719-956-683762
4	15.8	65.8	25	8	US-10-719-900-83698
5	15.8	65.8	25	8	US-10-719-900-743593
6	15.8	65.8	25	8	US-10-719-900-904575
7	15.8	65.8	25	8	US-10-719-900-979803
8	15.6	65.0	25	10	US-11-036-317-296939
9	15.6	65.0	25	10	US-11-036-317-498568
10	15.6	65.0	25	10	US-11-036-317-810975
11	15.6	65.0	26	8	US-10-874-242-35
12	15.2	63.3	25	8	US-10-719-900-741411
13	15.2	63.3	25	8	US-10-719-900-841215
14	15.2	63.3	25	9	US-10-809-189-92895
15	15.2	63.3	25	10	US-11-036-317-523845
16	15	62.5	25	8	US-10-719-900-599645
17	15	62.5	25	9	US-10-809-189-57613
18	15	62.5	25	9	US-10-956-157-14605
19	14.8	61.7	25	7	US-10-719-956-2771
20	14.8	61.7	25	7	US-10-719-956-692355
21	14.8	61.7	25	8	US-10-719-900-648791
22	14.8	61.7	25	9	US-10-956-157-315950
23	14.8	61.7	25	10	US-11-036-317-436639

Sequence 198953,
Sequence 198954,
Sequence 58299, A
Sequence 267621,
Sequence 267622,
Sequence 14604, A
Sequence 14606, A
Sequence 81764, A
Sequence 189892,
Sequence 552223,
Sequence 770140,
Sequence 1997, Ap
Sequence 520335,
Sequence 520337,
Sequence 46464, A
Sequence 183105,
Sequence 271344,
Sequence 272728,
Sequence 316163,
Sequence 336028,
Sequence 368993,
Sequence 372996,
Sequence 198953,
Sequence 198954,
Sequence 58299, A
Sequence 267621,
Sequence 267622,
Sequence 14604, A
Sequence 14606, A
Sequence 81764, A
Sequence 189892,
Sequence 552223,
Sequence 770140,
Sequence 1997, Ap
Sequence 520335,
Sequence 520337,
Sequence 46464, A
Sequence 183105,
Sequence 271344,
Sequence 272728,
Sequence 316163,
Sequence 336028,
Sequence 368993,
Sequence 372996,

ALIGNMENTS

RESULT 1
US-10-713-137-3
; Sequence 3, Application US/10713137
; Publication No. US20050106573A1
; GENERAL INFORMATION:
; APPLICANT: Pasha, Abdul Qadar Mohammad
; APPLICANT: Ahsan, Aarif
; TITLE OF INVENTION: A method of detection of predisposition
; FILE REFERENCE: 09755-0018051
; CURRENT APPLICATION NUMBER: US/10713.137
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-713-137-3

Query Match 100.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGACG 24
|||
Db 1 GATGCACAGCTGGGGAACAAGACG 24

RESULT 2
US-11-036-317-523844
; Sequence 523844, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```
; SEQ ID NO 523844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-523844

Query Match          70.0%; Score 16.8; DB 10; Length 25;
Best Local Similarity 90.0%; Pred. No. 8e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGAACAA 20
    |||||
Db 6 GCTGCACAGCTGAGGACAA 25

RESULT 3
US-10-719-956-683762/c
; Sequence 683762, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 683762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-683762

Query Match          65.8%; Score 15.8; DB 7; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAA 20
    |||||
Db 19 ATGCACAGCTGGGGTACAA 1

RESULT 4
US-10-719-900-83698/c
; Sequence 83698, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 83698
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-83698

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAGAC 23
    |||||
Db 24 CACAGCTGGGAATCAAGAC 6

RESULT 5
US-10-719-900-743593/c
; Sequence 743593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 743593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-743593

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCACAGCTGGGGAACAA 22
    |||||
Db 25 GCACAGATGGGCACAA 7

RESULT 6
US-10-719-900-904575/c
; Sequence 904575, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-904575

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAGAC 23
    |||||
Db 20 CACAGCTGGGGATGAAGAC 2

RESULT 7
US-10-719-900-979803/c
; Sequence 979803, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979803
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-979803

Query Match      65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22
Db 22 GCACAGATGGGCAACAAGA 4

RESULT 8
US-11-036-317-296939/c
; Sequence 296939, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 296939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-296939
```

```
Query Match      65.0%; Score 15.6; DB 10; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGAC 23
Db 25 ATGCTCATCTGTGGACCAAGAC 4
```

```
RESULT 9
US-11-036-317-498568
; Sequence 498568, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 498568
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-498568
```

```
Query Match      65.0%; Score 15.6; DB 10; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGA 22
Db 4 GCTGCACCTGCTGAGGAACAACA 25
```

```
RESULT 10
US-11-036-317-810975
; Sequence 810975, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 810975
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-810975
```

```
Query Match      65.0%; Score 15.6; DB 10; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAACAAGACG 24
Db 1 TGCTCAGCACTGGGAACAAGACG 22
```

```
RESULT 11
US-10-874-242-35
; Sequence 35, Application US/10874242
; Publication No. US20050026252A1
; GENERAL INFORMATION:
; APPLICANT: ESTES, SCOTT
; TITLE OF INVENTION: NOVEL PROMOTERS AND USES THEREOF
; FILE REFERENCE: 07680.0027-00000
; CURRENT APPLICATION NUMBER: US/10/874,242
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/480,768
; PRIOR FILING DATE: 2003-06-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: forward primer for amplifying beta-actin promoter containing
; OTHER INFORMATION: Intron 1
US-10-874-242-35
```

```
Query Match      65.0%; Score 15.6; DB 8; Length 26;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGAC 23
Db 1 AGGCCAGCTTGGGACCAAGAC 22
```

```
RESULT 12
US-10-719-900-741411/c
; Sequence 741411, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
```



```
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 741411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-741411
```

```
Query Match 63.3%; Score 15.2; DB 8; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 22 GATGCCCATCTTGGGAACAA 3
```

```
RESULT 13
US-10-719-900-841215/c
; Sequence 841215, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 841215
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841215
```

```
Query Match 63.3%; Score 15.2; DB 8; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 TGCACACAGCTGGGGAACAGA 22
    ||||| ||||| ||||| ||||| |||||
Db 20 TGCACAGCTAGGAAGAAAGA 1
```

```
RESULT 14
US-10-809-189-92895
; Sequence 92895, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-92895
```

```
Query Match 63.3%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 4 GCTGCAGAGCTGGGGAGAA 23
```

```
RESULT 15
US-11-036-317-523845
; Sequence 523845, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 523845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-523845
```

```
Query Match 63.3%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 6 GCTGCACCTGCTGAGGAGACAA 25
```

```
RESULT 16
US-10-719-900-599645
; Sequence 599645, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 599645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-599645
```

```
Query Match 62.5%; Score 15; DB 8; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAAAGAC 23
    ||||| ||||| ||||| ||||| |||||
Db 2 GAGGCAGAGCTGGGTACCAACAC 24
```

```
RESULT 17
US-10-809-189-57613/c
; Sequence 57613, Application US/10809189
; Publication No. US20050048531A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-57613

Query Match      62.5%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 ATGCACAGCTGGGGAACAAGACG 24
Db      23 ATGCAGAAATAGGGGAACAAGATG 1

RESULT 18
US-10-956-157-14605/c
; Sequence 14605, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14605
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14605

Query Match      62.5%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAACAAGAC 23
Db      23 GATTCACACCTGAGAAACAAGTC 1

RESULT 19
US-10-956-2771/c
; Sequence 2771, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-648791

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAC 18
Db      18 GATGCACAGCTGGGGACC 1

; GENERAL INFORMATION:
; APPLICANT: Rattus norvegicus
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-692355

Query Match      61.7%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ACAGCTGGGGAACAAGAC 23
Db      22 ACAGATGGAGACAAGAC 5

RESULT 20
US-10-719-956-692355/c
; Sequence 692355, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-692355

Query Match      61.7%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 CACAGCTGGGGAACAAGA 22
Db      20 CAAAGCTGGTGAACAAGA 3

RESULT 21
US-10-719-900-648791/c
; Sequence 648791, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-648791

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAC 18
Db      18 GATGCACAGCTGGGGACC 1
```

```
; SEQ ID NO 198953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198953

Query Match          60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred.No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3   TGCACAGCTGGGGAACAAGAC 23
         |||||
Db       24   TGCACAGCTGGTCAAGATGAC 4

RESULT 25
US-10-719-956-198954/c
; Sequence 198954, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198954
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198954

Query Match          60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred.No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3   TGCACAGCTGGGGAACAAGAC 23
         |||||
Db       24   TGCACAGCTGGCACAAGATGAC 4

RESULT 26
US-10-719-900-58299/c
; Sequence 58299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 58299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-58299

Query Match          60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred.No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3   TGCACAGCTGGGGAACAAGAC 23
         |||||
Db       24   TGCACAGCTGGGTCAAGATC 4
```

```
RESULT 27
US-10-719-900-267621/c
; Sequence 267621, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-267621

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3  TGCACAGCTGGGGAACAAGAC 23
Db      24  TGCACAGCTGGTCAAGAGGAC 4

RESULT 28
US-10-719-900-267622/c
; Sequence 267622, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-267622

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3  TGCACAGCTGGGGAACAAGAC 23
Db      24  TGCACAGCTGGTCAAGAGGAC 4

RESULT 29
US-10-956-157-14604/c
; Sequence 14604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14604
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14604

Query Match      60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GATGCACAGCTGGGGAACAAG 21
Db      21  GATTCACACCTGAGAAACAAG 1

RESULT 30
US-10-956-157-14606/c
; Sequence 14606, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14606
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14606

Query Match      60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GATGCACAGCTGGGGAACAAG 21
Db      22  GATTCACACCTGAGAAACAAG 2

RESULT 31
US-11-036-317-81764
; Sequence 81764, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81764
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-81764

Query Match      60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ATGCACAGCTGGGGAACAAGA 22
Db      3  AGGCACAGCTGGATAGCAAGA 23
```

```
RESULT 32
US-11-036-317-189892/c
; Sequence 189892, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 189892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-189892
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 TGCACAGCTGGGGAACAAGAC 23
Db 25 TGCATCTGTGGACCAAGAC 5
RESULT 33
US-11-036-317-552223
; Sequence 552223, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 552223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-552223
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ATGCACAGCTGGGGAACAAGA 22
Db 3 AGGCACAGCTGGATAGCAAGA 23
RESULT 34
US-11-036-317-770140/c
; Sequence 770140, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
```

```
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 770140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-770140
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ATGCACAGCTGGGGAACAAGA 22
Db 25 AAGCACAGCTGGTAAGAGGA 5
RESULT 35
US-10-349-143-1997
; Sequence 1997, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1997
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7877-363 : polymorphic base A or G
US-10-349-143-1997
Query Match 60.8%; Score 14.6; DB 6; Length 47;
Best Local Similarity 73.9%; Pred. No. 8.2e+03;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 GATGCACAGCTGGGGAACAAGAC 23
Db 24 RATGCACACCTGTTTCACAAGAC 46
RESULT 36
US-10-719-900-520335
; Sequence 520335, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520335
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-520335

Query Match      60.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGC 24
    |||||
Db 1 GATTCACAGCCGAGGACAGCAGG 24

RESULT 37
US-10-719-900-520337
; Sequence 520337, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520337
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-520337

Query Match      60.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGC 24
    |||||
Db 1 GATTCACAGCCGAGGACAGCAGG 24

RESULT 38
US-11-036-317-46464/c
; Sequence 46464, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46464
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-46464

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAC 18
    |||||
Db 25 TGCACAGCTGGGGATC 10

RESULT 39
US-11-036-317-183105/c
; Sequence 183105, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 183105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-183105

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAAGA 22
    |||||
Db 18 CAGCTGGGGAACAAGA 3

RESULT 40
US-11-036-317-271344/c
; Sequence 271344, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 271344
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-271344

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAAGA 22
    |||||
Db 17 CAGCTGGGGAACAAGA 2

Search completed: December 13, 2005, 16:17:15
Job time : 661 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:14:34 ; Search time 104.5 Seconds
(without alignments)
408.244 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatcacagctggggaacagacg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
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9: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15.2	63.3	25	3	US-09-396-196G-92895
2	15	62.5	25	3	US-09-396-196G-57613
3	15	62.5	38	2	US-08-537-811-13
4	14.6	60.8	47	3	US-09-422-978-1997
5	14.2	59.2	25	3	US-09-396-196G-103166
6	14.2	59.2	50	3	US-10-131-827-6696
7	14.2	59.2	50	3	US-10-131-827-7086
8	14	58.3	25	3	US-09-396-196G-32344
9	14	58.3	47	3	US-09-422-978-1898
10	14	58.3	50	3	US-10-131-827-6394
11	14	58.3	50	3	US-10-131-827-6784
12	13.8	57.5	17	3	US-09-866-108A-8469
13	13.8	57.5	20	3	US-09-194-478-5
14	13.8	57.5	25	3	US-09-866-108A-13361
15	13.8	57.5	25	3	US-09-866-108A-13362
16	13.8	57.5	25	3	US-09-866-108A-13363
17	13.8	57.5	25	3	US-09-866-108A-13364
18	13.8	57.5	25	3	US-09-866-108A-13365
19	13.8	57.5	25	3	US-09-866-108A-13366
20	13.8	57.5	25	3	US-09-866-108A-13367
21	13.8	57.5	25	3	US-09-866-108A-13368
22	13.8	57.5	25	3	US-09-866-108A-13369
23	13.8	57.5	47	3	US-09-422-978-3853
24	13.6	56.7	25	3	US-09-396-196G-57614

25	13.6	56.7	27	3	US-09-101-927-5	Sequence 5, Appli
26	13.6	56.7	31	3	US-08-679-645-361	Sequence 361, App
27	13.6	56.7	34	3	US-09-644-858-6	Sequence 6, Appli
28	13.6	56.7	49	3	US-09-220-557-11	Sequence 11, Appl
29	13.6	56.7	49	3	US-10-219-227-11	Sequence 11, Appl
30	13.4	55.8	25	3	US-09-396-196G-88421	Sequence 88421, A
31	13.4	55.8	25	3	US-09-396-196G-95727	Sequence 95727, A
32	13.4	55.8	25	3	US-09-396-196G-107466	Sequence 107466,
33	13.4	55.8	30	3	US-09-033-333-17	Sequence 17, Appl
34	13.4	55.8	30	3	US-09-033-428-18	Sequence 18, Appl
35	13.4	55.8	30	3	US-09-033-556-40	Sequence 40, Appl
36	13.4	55.8	30	3	US-09-614-495-17	Sequence 17, Appl
37	13.4	55.8	30	3	US-09-898-883-18	Sequence 18, Appl
38	13.4	55.8	30	3	US-08-462-159B-6	Sequence 6, Appli
39	13.4	55.8	30	3	US-09-814-292-38	Sequence 38, Appl
40	13.4	55.8	30	3	US-09-875-228-24	Sequence 24, Appl
41	13.4	55.8	45	3	US-09-897-259C-6	Sequence 6, Appli
42	13.4	55.8	47	3	US-09-338-907-332	Sequence 332, App
43	13.4	55.8	47	3	US-09-218-207-332	Sequence 332, App
44	13.2	55.0	25	3	US-09-396-196G-14507	Sequence 14507, A
45	13.2	55.0	25	3	US-09-396-196G-22239	Sequence 22239, A

ALIGNMENTS

RESULT 1

US-09-396-196G-92895
; Sequence 92895, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-92895

Query Match 63.3%; Score 15.2; DB 3; Length 25;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GATGCACAGCTGGGGAACAA 20
|||||
Db 4 GCTGCAGAGCTGGGGAAGAA 23

RESULT 2

US-09-396-196G-57613/c
; Sequence 57613, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

Query Match 59.2%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels


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US-10-131-827-6394
; Sequence 6394, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: CHRONIC INFLAMMATORY DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6394
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6394

Query Match      58.3%; Score 14; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGGGAACAAGA 22
    |||||
DB 31 GCTGGGGAACAAGA 44

RESULT 11
US-10-131-827-6784/c
; Sequence 6784, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: CHRONIC INFLAMMATORY DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6784
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6784

Query Match      58.3%; Score 14; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGGGAACAAGA 22
    |||||
DB 20 GCTGGGGAACAAGA 7

RESULT 12
US-09-866-108A-8469
; Sequence 8469, Application US/09866108A
; Patent No. 6686188
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US-10-131-827-6394
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aeoica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8469
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8469

Query Match      57.5%; Score 13.8; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGCG 24
    |||||
DB 1 AGCTGGGGAACAAGCG 17

RESULT 13
US-09-194-478-5/c
; Sequence 5, Application US/09194478
; Patent No. 6284463
; GENERAL INFORMATION:
; APPLICANT: Hasebe, Masahisa
; APPLICANT: Goto, Masanori
; APPLICANT: Tosu, Mariko
; TITLE OF INVENTION: Method for Detection of Mutations
; FILE REFERENCE: PU96-1684
; CURRENT APPLICATION NUMBER: US/09/194,478
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: PCT/SE97/00839
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: SWEDEN 9602062-3
; PRIOR FILING DATE: 1996-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: synthetic construct
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US-09-194-478-5

Query Match 57.5%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAACAAGA 22
||||||| |||||
Db 20 ACAGCTGGGGAAGAAGA 4

RESULT 14

US-09-866-108A-13361
; Sequence 13361, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13361

Query Match 57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
||||||| |||||
Db 9 AGCTGGGGAACAATGACG 25

RESULT 15

US-09-866-108A-13362
; Sequence 13362, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13361

Query Match 57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
||||||| |||||
Db 9 AGCTGGGGAACAATGACG 25

RESULT 15

US-09-866-108A-13362
; Sequence 13362, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13362

Query Match 57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
||||||| |||||
Db 8 AGCTGGGGAACAATGACG 24

RESULT 16

US-09-866-108A-13363
; Sequence 13363, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13363

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
Db      7 AGCTGGAGAATGACG 23

RESULT 17
US-09-866-108A-13364
; Sequence 13364, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13364
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13365

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
Db      7 AGCTGGAGAATGACG 23

RESULT 18
US-09-866-108A-13365
; Sequence 13365, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13365

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
Db      5 AGCTGGAGAATGACG 21

RESULT 19
US-09-866-108A-13366
; Sequence 13366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```

```
; ORGANISM: Homo sapiens
US-09-866-108A-13364

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
Db      6 AGCTGGAGAATGACG 22

RESULT 18
US-09-866-108A-13365
; Sequence 13365, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13365

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
Db      5 AGCTGGAGAATGACG 21

RESULT 19
US-09-866-108A-13366
; Sequence 13366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```

```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13366

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGAGACATGACG 20

RESULT 20
US-09-866-108A-13367
; Sequence 13367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13366

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGAGACATGACG 20

RESULT 20
US-09-866-108A-13367
; Sequence 13367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13367

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      3 AGCTGGAGACATGACG 19

RESULT 21
US-09-866-108A-13368
; Sequence 13368, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13368
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13368

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AGCTGGGGGAACAGACG 24
    ||||| ||||| |||||
Db 2 AGCTGGAGAACATGACG 18

RESULT 22
US-09-866-108A-13369
; Sequence 13369, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13369
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13369

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGGAACAGACG 24
    ||||| ||||| |||||
Db 1 AGCTGGAGAACATGACG 17

RESULT 23
US-09-422-978-3853/c
; Sequence 3853, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Rickles, Richard J
; TITLE OF INVENTION: Cell-Based Assay
; FILE REFERENCE: 336A PCT/US
```


Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAAGACG 24
||||| ||||| ||||| ||
Db 39 CACAGCGAGGGAGCAAGTCG 20

RESULT 29

US-10-219-227-11/c
; Sequence 11, Application US/10219227
; Patent No. 6891086
; GENERAL INFORMATION:
; APPLICANT: Oakes, Janette V.
; APPLICANT: Chaudhuri, Sumita
; TITLE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA
; FILE REFERENCE: 15398/01/US
; CURRENT APPLICATION NUMBER: US/10/219,227
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US/09/465,856
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/220,557
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-219-227-11

Query Match 56.7%; Score 13.6; DB 3; Length 49;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAAGACG 24
||||| ||||| ||||| ||
Db 39 CACAGCGAGGGAGCAAGTCG 20

RESULT 30

US-09-396-196G-88421
; Sequence 88421, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88421
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88421

Query Match 55.8%; Score 13.4; DB 3; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.1e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGACG 24
||||| ||||| ||||| ||
Db 1 ATGGCTCTTGGGGACAATCG 23

RESULT 31

US-09-396-196G-95727
; Sequence 95727, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95727
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-95727

Query Match 55.8%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 6.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAA 17
||| ||||| ||||| ||
Db 7 TGAACAGCTGGGGAA 21

RESULT 32

US-09-396-196G-107466/c
; Sequence 107466, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107466
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107466

Query Match 55.8%; Score 13.4; DB 3; Length 25;
Best Local Similarity 73.9%; Pred. No. 6.1e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGACG 24
||| ||||| ||||| ||
Db 25 ATTCACAGCTGTTTAAAAAGAGG 3

RESULT 33

US-09-033-333-17/c
; Sequence 17, Application US/09033333
; Patent No. 6197293
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel

```
;
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,333
; FILING DATE: 02-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-333-17
;
; Query Match 55.8%; Score 13.4; DB 3; Length 30;
; Best Local Similarity 73.9%; Pred. No. 6.3e+03;
; Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; QY 2 ATGCACAGCTGGGGAACAGAGC 24
; DB 25 AAGCAGCGGTGGGAACAAAGG 3
;
; RESULT 34
; US-09-033-428-18/c
; Sequence 19, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-428-18
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; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-428-18
;
; Query Match 55.8%; Score 13.4; DB 3; Length 30;
; Best Local Similarity 73.9%; Pred. No. 6.3e+03;
; Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
;
; QY 2 ATGCACAGCTGGGGAACAGAGC 24
; DB 25 AAGCAGCGGTGGGAACAAAGG 3
;
; RESULT 35
; US-09-033-556-40/c
; Sequence 40, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-556-40
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Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
   ||||| ||||| ||||| ||||| |||||
Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 36
US-09-614-495-17/c
; Sequence 17, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-614-495-17

Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
   ||||| ||||| ||||| ||||| |||||
Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 37
US-09-898-883-18/c
; Sequence 18, Application US/09898883
; Patent No. 6585968
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,883
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-898-883-18

Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
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Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 38
US-08-462-159B-6/c
; Sequence 6, Application US/08462159B
; Patent No. 6787640
; GENERAL INFORMATION:
; APPLICANT: Greene Ph.D., John M.
; APPLICANT: Dillon Ph.D., Patrick J.
; TITLE OF INVENTION: Fibroblast Growth Factor 14
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,159B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,412
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-462-159B-6

Query Match 55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGC 24
Db 23 ACGCGCCGCTGGGGATCCAGTCG 1

RESULT 39

US-09-814-292-38/c
; Sequence 38, Application US/09814292
; Patent No. 6852528
; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer 37,124.3
US-09-814-292-38

Query Match 55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGC 24
Db 25 AAGCAGAGCGGTGGAAACAAAGG 3

RESULT 40

US-09-875-228-24/c
; Sequence 24, Application US/09875228
; Patent No. 6916918
; GENERAL INFORMATION:

; APPLICANT: Yu, D.
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022000900
; CURRENT APPLICATION NUMBER: US/09/875,228
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/127,834
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/076,545
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/054,523
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence is
; Patent No. 6916918
; OTHER INFORMATION: produced synthetically.
US-09-875-228-24

Query Match 55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGC 24
Db 25 AAGCAGAGCGGTGGAAACAAAGG 3

Search completed: December 13, 2005, 15:55:00
Job time : 105.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:51:49 ; Search time 2984 Seconds
(without alignments)
376.304 Million cell updates/sec

Title: US-10-713-137-3
Perfect score: 24
Sequence: 1 gatcacagctgggggaacaagacg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 3	14.6	60.8	46	11	CR396399	Arabidops
C 4	14	58.3	38	10	AL945338	Arabidops
C 5	14	58.3	50	1	AU1033763	Arabidops
C 6	13.6	56.7	39	9	AZ769231	1M0569G07
7	13.2	55.0	31	1	AI156750	ue54b07.r
C 8	13	54.2	38	10	CL844510	EY12606-5
C 9	13	54.2	41	9	AZ470528	1M0284H11
C 10	13	54.2	43	1	AI185696	ge60g07.x
C 11	13	54.2	43	10	CS803673	1118044H1
C 12	13	54.2	50	1	AU1033768	AU1033768
C 13	13	54.2	50	1	AU104109	AU104109
C 14	13	54.2	50	9	AZ565607	211PVA09
C 15	12.8	53.3	42	9	BH865278	SALK 0980
C 16	12.8	53.3	47	1	AV832547	AV832547
C 17	12.6	52.5	30	10	AG200388	Pan trogl
C 18	12.6	52.5	43	10	CZ472331	d01604-3p
C 19	12.6	52.5	47	10	AG217348	Drosophil
C 20	12.6	52.5	49	1	AI527771	uJ28H01.Y
C 21	12.4	51.7	25	9	AZ511249	1M0356N10
C 22	12.4	51.7	28	1	AA958372	uall1a03.r

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24	12.4	51.7	42	9	AZ814914	2M0082C24
25	12.4	51.7	45	9	BH855497	BH855497 SALK 0850
26	12.4	51.7	48	9	BH626386	1007113H0
C 27	12.4	51.7	49	9	BH640991	1008039E0
28	12.4	51.7	49	10	CZ469449	CZ469449 c04702-3p
C 29	12.2	50.8	18	3	BM395302	BM395302 50072-2-8
C 30	12.2	50.8	36	1	AA776443	AA776443 zj50h10.s
C 31	12.2	50.8	37	1	AJ239879	AJ239879 AJ239879
C 32	12.2	50.8	41	1	AA287473	AA287473 zs50a12.r
C 33	12.2	50.8	42	1	AV957763	AV957763 AV957763
C 34	12.2	50.8	44	1	AU255694	AU255694 AU255694
C 35	12.2	50.8	45	1	AJ792767	AJ792767 AJ792767
C 36	12.2	50.8	49	1	AI254367	AI254367 qv33a10.x
C 37	12.2	50.8	50	1	AU105506	AU105506 AU105506
C 38	12.2	50.8	50	1	AU105507	AU105507 AU105507
C 39	12	50.0	30	10	CZ909855	CZ909855 4018011H1
C 40	12	50.0	33	8	DN955268	DN955268 it84h05.g
C 41	12	50.0	38	8	R10392	R10392 Yf37e03.81
C 42	12	50.0	38	9	CC798667	CC798667 SALK 1472
C 43	12	50.0	38	9	CC798676	CC798676 SALK 1472
C 44	12	50.0	39	9	AZ501408	AZ501408 1M0340813
C 45	12	50.0	40	10	AG199766	AG199766 Pan trogl

ALIGNMENTS

RESULT 1
CL214453
LOCUS W255E01 GGTCT Gene Trap Library GV04C04 Mus musculus linear GSS 22-MAR-2005
DEFINITION W255E01, mRNA sequence.
ACCESSION CL214453.2 GI:49489711
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hansen, J., Flose, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
TITLE A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
PUBMED 12904583
COMMENT On Jan 27, 2005 this sequence version replaced gi:40731354.
Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
ROSAbetago+1 Gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=W255E01'. ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm 1'. Inhouse Sequence Identifier: 12462
Class: Gene Trap.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="W255E01"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV04C04"
/note="Vector: ROSAbetago"

ORIGIN

Query Match	62.5%	Score 15	DB 10	Length 30
Best Local Similarity	78.3%	Pred. No. 5.2e+04		
Matches 18	Conservative 0	Mismatches 5	Indels 0	Gaps 0

RESULT 2	AZ8323358/c
LOCUS	AZ8323358
DEFINITION	2M0112P1OR Mouse 10kb plasmid UGCGN library Mus musculus genomic clone UGC2M0112P10 R, genomic survey sequence.
ACCESSION	AZ8323358
VERSION	AZ832358.1
	GI:13002266
	37 bp DNA linear GSS 20-FEB-2001

SOURCE	ORGANISM
Mus musculus (house mouse)	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 37)

1 (bases 1 to 37)

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

JOURNAL COMMENT
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: P column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.

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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112P10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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ORIGIN

Query Match	60.8%	Score 14.6	DB 9	Length 37
Best Local Similarity	81.0%	Pred No. 7	9e+04	
Matches 17	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Qy	4	GCACAGCTGGGGAACAGAGCG	24	
Db	27	GCAGAGCTGGAGGACCAAGTCG	7	

RESULT 3
CR396399/c
LOCUS
DEFINITION
CR396399 46 bp DNA linear GSS 01-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-198G05-025984,
genomic survey sequence.

CR396399
 CR396399.1 GI:46936982
 GSS.
 Arabidopsis thaliana (thale cress)

SOURCE	<i>Arabidopsis thaliana</i> (thale cress)
ORGANISM	<i>Arabidopsis thaliana</i>
	Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; Magnoliophyta (eudicotyledons); Rosales; Brassicales; Arabidopsida I; Arabidopsidae; Arabidopsini; <i>Arabidopsis</i>

REFERENCE

AUTHORS	Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE	GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED	12874060
REFERENCE	2
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED	14756321

REFERENCE	3	Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.
TITLE		High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL		BioTechniques 35 (6), 1164-1168 (2003)
PUBMED		14682050
REFERENCE	4	(bases 1 to 46)
AUTHORS		Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
TITLE		Direct Submission
JOURNAL		Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT		This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At1g03160. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPIZ for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

```

1. .46
source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-198G05-025984"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (Ti) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

```

ORIGIN

Query Match 60.8%; Score 14.6; DB 11; Length 46;
 Best Local Similarity 81.0%; Pred. No. 8e+04; 4; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGA 22
 ||||| ||||| ||||| |||||
 Db 45 ACGCACAGCTGGGGAACAAGA 25

RESULT 4

AL945338/c
 LOCUS AL945338 38 bp DNA linear GSS 01-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-288F04-015346,
 genomic survey sequence.

ACCESSION AL945338
 VERSION AL945338.1 GI:24401960
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weissshaar, B.
 TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse Genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050

REFERENCE Li, Y., Rosso, M.G., Strizhov, N. and Weissshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 F5D14. Details on the protocols used for generation of the sequence
 are described in References 1-3. The sequences are generated at the
 MPI for Plant Breeding Research in the context of the GABI-Kat
 project. GABI-Kat is part of the German Plant Genomics program
 designated 'GABI'. Information on line availability can be found
 at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..38

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-288F04-015346"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 58.3%; Score 14; DB 10; Length 38;
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGA 22
 ||||| ||||| ||||| |||||
 Db 33 GATGCACACAGCGGATCACA 12

RESULT 5

AU103763/c
 LOCUS AU103763 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 HEP10745, mRNA sequence.

ACCESSION AU103763
 VERSION AU103763.1 GI:13553284
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 PUBMED 11375929

COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yszuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES

source

1..50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HEP10745"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 58.3%; Score 14; DB 1; Length 50;
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGAC 23
 ||||| ||||| ||||| |||||
 Db 25 AGGCTAGCTGGCGAACAACAC 4

RESULT 6

AZ769231/c
 LOCUS AZ769231 39 bp DNA linear GSS 16-FEB-2001
 DEFINITION LM0569G07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0569G07 R, genomic survey sequence.

ACCESSION AZ769231
 VERSION AZ769231.1 GI:12889151
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 39)

AUTHORS
Dunn, D., Royagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0569 row: G column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
1..39

FEATURES
source
1..39
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M056907"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1/4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 56.7%; Score 13.6; DB 9; Length 39;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAAGACG 24
|||||
DB 33 CACAGTTAGGTACAAAGATG 14
|||||

RESULT 7
A1156750
LOCUS
DEFINITION
A1156750.1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1494901 5' similar to TR:Q99942 Q99942 HYPOTHETICAL 19.9 KD PROTEIN ;, mRNA sequence.
A1156750 31 bp mRNA linear EST 30-SEP-1998
A1156750.1 GI:3685219
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Suarchontoglires; Glires; Rodentia;

REFERENCE

AUTHORS

Sciurognathi: Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LILNL ; contact the IMAGE Consortium (info@image.lilnl.gov) for further information.
MGI:932505
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1494901"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

ORIGIN

Query Match 55.0%; Score 13.2; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CAGCTGGGGAACAAGACG 24
|||||
DB 6 CAGCAGAGGAGAGACG 23
|||||

RESULT 8

LOCUS

DEFINITION

CL844510 38 bp DNA linear GSS 09-AUG-2004
EY12606-5prime Drosophila melanogaster P[EPgy2] P element insertion lines Drosophila melanogaster genomic sequence recovered from 5' end of P element, genomic survey sequence.
CL844510
CL844510.1 GI:51090120
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 38)
Levis, R., Hoskins, R., Liao, G., Morden, N., Tsang, G., He, Y., Karpis, G., Bellen, R., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project

University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106433947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1. 38
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P{EPgy2} P element insertion lines"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P{EPgy2} P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://www.fruitfly.org/about/methods/inverse.pcr.html>."

ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 38;
Best Local Similarity 76.2%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGA 22

Db 29 ATGAAGAAGCTGCATAACAAGA 9

RESULT 9

AZ470528/c
LOCUS 41 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0284H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0284H1 R, genomic survey sequence.

ACCESSION AZ470528

VERSION AZ470528.1 GI:10628653

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 41)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0284 row: H column: 11

Seq primer: CACACAGGACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1. 41

/organism="Mus musculus"

FEATURES

source

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0284H1"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 41;
Best Local Similarity 76.2%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGACAGACG 24

Db 40 GCACAGCGGGGGCCAGGATG 20

RESULT 10

AT185696/c

LOCUS 43 bp mRNA linear EST 29-OCT-1998

DEFINITION Q66097.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1743420 3' similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO 1, mRNA sequence.

ACCESSION AT185696

VERSION AT185696.1 GI:3736334

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 43)

NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 612 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. 43

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1743420"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares_fetal_lung_NBHL19W"

FEATURES

source

/note="Organ: lung; Vector: pTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GTGACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHH19W."

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 43;
Best Local Similarity 76.2%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGNACAAG 21
||||| | | | | | | | | | | | | | | | | | | | |
Db 23 GATGCCCGCCGGGGNAAAAG 3

RESULT 11

CG803673 43 bp DNA linear GSS 10-NOV-2003
DEFINITION 1118044H12.2EL.Y1 1118 - RescueMu Grid S Zea mays genomic, genomic survey sequence.

ACCESSION CG803673
VERSION CG803673.1 GI:38239459
KEYWORDS GSS.

SOURCE

Zea mays
Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

COMMENTS

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118044 row: 14
Class: transposon-tagged.
Location/Qualifiers
1. .43
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES

source

ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 43;
Best Local Similarity 76.2%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGNACAAG 21
||||| | | | | | | | | | | | | | | | | | | | |
Db 11 GATGAACAGATGTGGAGATG 31

RESULT 12

AU103768/c
LOCUS AU103768 Sugano Homo sapiens cDNA library EST 28-JAN-2004
DEFINITION HEPI2651, mRNA sequence.

ACCESSION AU103768
VERSION AU103768.1 GI:13553289
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Seae, J., Hata, H., Ota, T., Isogai, T., Tanaka, I., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

PUBMED

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEPI2651"
/clone_lib="Sugano Homo sapiens cDNA library"

FEATURES

source

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 4.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 GCACAGCTGGGGNACAAGACG 24
||||| | | | | | | | | | | | | | | | | | | | |
Db 26 GAACCACTTGGAAAGAGACG 6

RESULT 13

AU104109/c
LOCUS AU104109 Sugano Homo sapiens cDNA library EST 28-JAN-2004
DEFINITION HEPI3777, mRNA sequence.

ACCESSION AU104109
VERSION AU104109.1 GI:13553630
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsumoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isoqai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. fine, large-scale mapping of mRNA start sites

JOURNAL PUBMED EMBO Rep. 2 (5), 388-393 (2001) 11375929

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HEPI3777"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 54.2%; Score 13; DB 1; Length 50;
Best Local Similarity 76.2%; Pred. No. 4.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAG 21
|||||
Db 40 GGTGCAAGCTGAGCAACGAG 20
|||||

RESULT 14
AZ565607/c
LOCUS 211pA09 Pv MEN #16 (50 bp DNA linear GSS 07-MAY-2001)
DEFINITION 211pA09 Pv MEN #16 (amplified twice) Plasmodium vivax genomic 3', genomic survey sequence.

ACCESSION AZ565607
VERSION AZ565607.1 GI:13971874
KEYWORDS GSS.
SOURCE Plasmodium vivax (malaria parasite P. vivax)
ORGANISM Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 50)
Carlton, J.M.-R. and Dame, J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today 16 (10), 409 (2000)
PUBMED 11006469

COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
Class: shotgun.

FEATURES source
1..50
Location/Qualifiers
/organism="Plasmodium vivax"
/mol_type="genomic DNA"
/strain="Belem"
/db_xref="taxon:5855"
/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
/clone_lib="Pv MEN #16 (amplified twice)"
/note="Vector: Lambda ZAP II (Stratagene); individual clones excised into phagemid pBluescript; Site 1: Ecor I; Site 2: Ecor I; Genomic DNA was prepared from asynchronous blood stage forms of the Belem line of P. vivax grown in squirrel monkeys. Parasitized erythrocytes were purified

from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman Cfl1 cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formamide at 50°C as described (Galinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al.1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."

ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 50;
Best Local Similarity 76.2%; Pred. No. 4.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAG 21
|||||
Db 23 GAGGCATCTCTAGGGAACAAG 3
|||||

RESULT 15

BH865278
LOCUS 42 bp DNA linear GSS 05-AUG-2002
DEFINITION SALK_098078 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_098078, genomic survey sequence.

ACCESSION

BH865278

VERSION

BH865278.1 GI:22101176

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 42)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jecke, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At3g23970.

Class: TDNA tagged.

Location/Qualifiers

1..42

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone_lib="SALK_098078"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"**ORIGIN**

Query Match 53.3%; Score 12.8; DB 9; Length 42;
Best Local Similarity 70.8%; Pred. No. 5.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 GATGCACAGCTGGGGAACAGC 24
  |||||
Db 3 GAGGCACAGCTGTGAGACATGAAG 26
  |||||

RESULT 16
AV832547/c 47 bp mRNA linear EST 09-MAY-2002
LOCUS AV832547 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA
          clone baak12a18, mRNA sequence.
ACCESSION AV832547 GI:14524636
VERSION AV832547
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Poideae; Triticeae; Hordeum.
          1 (bases 1 to 47)
REFERENCE Sato, K.
AUTHORS Barley EST sequencing project in NIG and Okayama Univ
TITLE Unpublished (2001)
JOURNAL
COMMENT Contact: Kazuhiro Sato
          Research Institute for Bioresources
          Okayama University, Barley Germplasm Center
          Chujo 2-20-1, Kurashiki, Okayama 710-0046, Japan
          Email: kzsato@rib.okayama-u.ac.jp,
          URL: http://www.rib.okayama-u.ac.jp/barley/
          database: http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES
    source
    1..47
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Akashinriki"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baak12a18"
    /tissue_type="leaves"
    /dev_stage="vegetative stage"
    /clone_lib="K. Sato unpublished cDNA library: Hordeum
    vulgare subsp. vulgare leaves vegetative stage"

ORIGIN
Query Match 53.3%; Score 12.8; DB 1; Length 47;
Best Local Similarity 77.8%; Pred. NO. 5.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACA 19
  |||||
Db 31 ATGGACAGCTGGGTANNA 14
  |||||

RESULT 17
AG200388 30 bp DNA linear GSS 06-MAR-2004
LOCUS AG200388 Pan troglodytes DNA, clone: RP43-082F17.T7, genomic survey
DEFINITION sequence.
ACCESSION AG200388 GI:45232563
VERSION AG200388
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Pan.
          1
REFERENCE Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
AUTHORS Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30)
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

QY 1 GATGCACAGCTGGGGAACA 19
  |||||
Db 3 GATGCACAGCTGAGGTACA 21
  |||||

RESULT 18
CZ472331/c 43 bp DNA linear GSS 29-APR-2005
LOCUS CZ472331 d01604-3prime Exelixis P element XP insertions Drosophila
DEFINITION melanogaster genomic Sequence recovered from 3' end of P element,
          genomic survey sequence.
ACCESSION CZ472331 GI:62966344
VERSION CZ472331.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
          1 (bases 1 to 43)
REFERENCE Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
AUTHORS Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
          Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
          Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,
          Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
          Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
          Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
          A complementary transposon tool kit for Drosophila melanogaster
          using P and piggyBac
          Nat. Genet. 36 (3), 283-287 (2004)
          14981521
JOURNAL
PUBMED Contact: Roger A Hoskins
COMMENT Berkeley Drosophila Genome Project
          Lawrence Berkeley National Laboratory
          Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
          Tel: 510 486 4015
          Fax: 510 486 6798
          Email: RHoskins@lbl.gov
          Sequence recovery method was inverse PCR.
          Sequence orientation is forward strand relative to 5' end of P
          element.
          The P element insertion position is 1 in the 43 bases. This

```

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/,
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43. This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.

PRIMERs
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI
 Location/Qualifiers
 1..30
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-082F17.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 52.5%; Score 12.6; DB 10; Length 30;
 Best Local Similarity 78.9%; Pred. NO. 6.4e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGAACA 19
 |||||
 Db 3 GATGCACAGCTGAGGTACA 21
 |||||

RESULT 18
 CZ472331/c 43 bp DNA linear GSS 29-APR-2005
 LOCUS CZ472331 d01604-3prime Exelixis P element XP insertions Drosophila
 DEFINITION melanogaster genomic Sequence recovered from 3' end of P element,
 genomic survey sequence.
 ACCESSION CZ472331 GI:62966344
 VERSION CZ472331.1
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 43)
 AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
 Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
 Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
 Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,
 Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
 Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster
 using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)

TITLE
 JOURNAL
 PUBMED 14981521
 COMMENT Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: RHoskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P
 element.
 The P element insertion position is 1 in the 43 bases. This

insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon insertion site.

FEATURES

source
Location/Qualifiers
1..43
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY1515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amminution element among inserts hopped onto the Bininscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 52.5%; Score 12.6; DB 10; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGACAAAGACG 24
||||| |||||
Db 22 ACAGCTGACAAACAAAGCCG 4

RESULT 19
AG217348/c
LOCUS
DEFINITION
AG217348 47 bp DNA linear GSS 03-SEP-2002
Drosophila melanogaster DNA, clone:NP3335-5-1, flanking P[GawB]
transposon insertion, genomic survey sequence.

ACCESSION
AG217348.1 GI:22764348
GSS.

KEYWORDS
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1
Hayashi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H.,
Aigaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R.,
Uemura,T., Yoshihara,M. and Goto,S.
GETDB, a database compiling expression patterns and molecular
locations of a collection of Gal4 enhancer traps
Genesis (2002) In press
2 (bases 1 to 47)
Hayashi,S.
Direct Submission
Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Singaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
(E-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
Fax:81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of
the P element vector P[GawB] of a Drosophila strain.

FEATURES
source
1..47
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP3335"
/db_xref="taxon:7227"
/chromosome="2"
/map="57B5"
/clone="NP3335-5-1"
/note="flanking P[GawB] transposon insertion"

ORIGIN

Query Match 52.5%; Score 12.6; DB 10; Length 47;
Best Local Similarity 78.9%; Pred. No. 6.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGACAAAGA 22
||||| |||||
Db 26 GAACAGCTGGCGCAGAAGA 8

RESULT 20
A1527771/c
LOCUS
DEFINITION
A1527771 49 bp mRNA linear EST 18-MAR-1999
U128ho1.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1931297 5' similar to TR:Q61314 Q61314 APOLIPOPROTEIN B ;
mRNA sequence.

ACCESSION
A1527771.1 GI:4441897
EST.

VERSION
A1527771.1
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 49)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:977589
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1931297"
/sex="female"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DralII
(CACTGTGTG); Site 2: DralII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DralII adaptor [TGTGGCCTACTGG], digested
and cloned into distinct DralII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constituted by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGTCTATAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."

ORIGIN

Query Match 52.5%; Score 12.6; DB 1; Length 49;
Best Local Similarity 78.9%; Pred. No. 6.6e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGACAA 20
 ||| ||| ||| ||| |||
 Db 39 ATACACAGAGGGGCAACAA 21

RESULT 21
 AZS11249/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

25 bp DNA linear GSS 05-OCT-2000
 1M0356N10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0356N10 F, genomic survey sequence.

AZS11249
 AZS11249.1 GI:10692565
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0356 row: N column: 10
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

FEATURES
 source
 1..25
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0356N10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 51.7%; Score 12.4; DB 9; Length 25;

Best Local Similarity 72.7%; Pred. No. 7.7e+05;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGACAAAGAC 23
 ||| ||| ||| ||| ||| |||
 Db 22 ACGAGCAGCGGGGAACACAAAC 1

RESULT 22
 AA958372
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

28 bp mRNA linear EST 08-MAY-1998
 uai1a03.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
 IMAGE:1346380 5' similar to TR:000111 O00111 HYPOTHETICAL 28.2DA
 PROTEIN FROM HUMAN CHROMOSOME 19. [1] ; mRNA sequence.

AA958372
 AA958372.1 GI:3124602
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HHMI Mouse EST Project
 Unpublished (1996)

JOURNAL
 COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 source
 1..28
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1346380"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland NbMMG"
 /note="Organ: mammary gland; Vector: p7T3D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5,
 TGTTACCAATCTGAAGTGGGCGCGGAATGTTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified p7T3D vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."

ORIGIN

Query Match 51.7%; Score 12.4; DB 1; Length 28;
 Best Local Similarity 92.9%; Pred. No. 7.8e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

Qy 1 CATGCACAGCTGGG 14
Db 2 GATGCAGCTGCTGGG 15

RESULT 23
LOCUS CW986355
DEFINITION KB-RH012L05R KBrH, Brassica rapa HindIII BAC library linear GSS 29-DEC-2004
subap. pekinensis genomic clone KBrH012L05, genomic survey
sequence.
ACCESSION CW986355
VERSION CW986355.1 GI:56852379
SOURCE GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 38)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.
TITLE End sequence of Brassica rapa HindIII BAC library (KBrH)
JOURNAL Unpublished (2004)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone
KBrH012L05
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..38
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH012L05"
/tissue_type="young leaves"
/lab_host="E.coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBacI; Site 1: HindIII; Brassica rapa
ssp. pekinensis inbred line Chifu BAC library (KBrH BAC)
is provided by Yong-Pyo Lim."

ORIGIN
Query Match 51.7%; Score 12.4; DB 10; Length 38;
Best Local Similarity 92.9%; Pred. No. 8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGGGAACAGAGG 24
Db 4 TGGGGAACAGAGG 17

RESULT 24
LOCUS AZ814914
DEFINITION 2M0082C24R Mouse 10kb plasmid UUGC1M library linear GSS 20-FEB-2001
clone UUGC2M0082C24 R, genomic survey sequence.
ACCESSION AZ814914
VERSION AZ814914.1 GI:12984822
SOURCE GSS.
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

Qy 1 (bases 1 to 42)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0882 row: C column: 24
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082C24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 51.7%; Score 12.4; DB 9; Length 42;
Best Local Similarity 72.7%; Pred. No. 8.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAGAC 23
Db 18 ATGCACAGGTGTGCAGGAGCC 39

RESULT 25
LOCUS BH855497
DEFINITION SALK_085040.16.20.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_085040.16.20.x, genomic
survey sequence.
ACCESSION BH855497
VERSION BH855497.1 GI:21705087
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```


Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 45)

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g09190.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..45

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_085040.16.20.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 45;
Best Local Similarity 72.7%; Pred. No. 8.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAAACAGAC 23

||||| | | | | | | | | | | | | | | | | |

DB 12 ATGCATACCTAGAGACGAGAC 33

RESULT 26

BH626386

LOCUS

DEFINITION 1007113406.1EL.x1 1007 - RescueMu Grid H Zea mays genomic, genomic

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 48)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1007113 column: 24

Class: transposon-tagged

Location/Qualifiers

FEATURES

source

1..48

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stages="adult"

/lab_host="DH10B"

/clone_lib="1007 - RescueMu Grid H"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI, Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid H was grown at Berkeley in 2001. DNA

was extracted from leaf punches, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 48;
Best Local Similarity 72.7%; Pred. No. 8.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GATCACAGCTGGGGAAACAAGA 22

||||| | | | | | | | | | | | | | | | | |

DB 25 GAAGGACAGCTGGAGGATAGGA 46

RESULT 27

BH640991/c

LOCUS

DEFINITION 1008039E08.1EL.x1 1008 - RescueMu Grid I Zea mays genomic, genomic

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 49)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008039 row: 29

Class: transposon-tagged.

Location/Qualifiers

source

1..49

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stages="adult"

/lab_host="DH10B"

/clone_lib="1008 - RescueMu Grid I"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI, Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 49;
Best Local Similarity 72.7%; Pred. NO. 8.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGACACAGCG 24
||||| ||| ||| ||| ||| |||
Db 42 TGCACAACCTTGACACCAAG 21

RESULT 28

CZ469449 49 bp DNA linear GSS 29-APR-2005

LOCUS c04702-3prime Exelixis piggyBac PB insertions Drosophila
DEFINITION melanogaster genomic Sequence recovered from 3' end of piggyBac,
genomic survey sequence.

ACCESSION CZ469449 GI:62963462

VERSION GSS.

KEYWORDS Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 49)

REFERENCE Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung L.N., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hautou, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: RHoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of

piggyBac element.

The piggyBac insertion position is 1 in the 49 bases. This

insertion position refers to the first base of the 4 base TTAA

target recognition sequence.

Class: transposon insertion site.

FEATURES

source

1..49

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strains="isogenic w- strain"

/db_xref="taxon:7227"

/clone_lib="Exelixis piggyBac PB insertions"

/note="Vector: piggyBac PB (GenBank accession number

AF151546); An isogenic w- Drosophila melanogaster strain

was mutagenized by remobilization of transposable

elements. We remobilized the PB element using

Hsp70:piggyBac transposase from a single ammunition

element on either the X or third chromosome. We induced

transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dyogenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 51.7%; Score 12.4; DB 10; Length 49;
Best Local Similarity 92.9%; Pred. NO. 8.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGA 16
||||| ||| ||| ||| |||
Db 11 TGCACACCTGGGGA 24

RESULT 29

BM395302/c

LOCUS BM395302

DEFINITION 50072-2-8-E01.r.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395302.1

VERSION GI:18195355

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 18)

REFERENCE Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3

location/Qualifiers

1..18

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 50.8%; Score 12.2; DB 3; Length 18;

Best Local Similarity 82.4%; Pred. NO. 9.3e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAACAAGA 22

||||| ||| ||| ||| |||

Db 17 ACAGCTGGGGGCCAAGA 1

||||| ||| ||| ||| |||

RESULT 30

AA776443

LOCUS AA776443

DEFINITION zj50h10.s1 Soares fetal liver spleen INFLS.S1 Homo sapiens CDNA

clone IMAGE:453763.3, similar to gb|L28107|TRRRRH Trichoderma

ressei 25S ribosomal (rRNA);, mRNA sequence.

36 bp mRNA linear EST 05-FEB-1998
zj50h10.s1 Soares fetal liver spleen INFLS.S1 Homo sapiens CDNA
clone IMAGE:453763.3, similar to gb|L28107|TRRRRH Trichoderma
ressei 25S ribosomal (rRNA);, mRNA sequence.

```

ACCESSION      AA776443
VERSION        AA776443.1  GI:2835777
SOURCE        EST.
KEYWORDS      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
TITLE         1 (bases 1 to 36)
JOURNAL       Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
COMMENT       Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
              Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
              Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
              WashU-NCI human EST Project
              Unpublished (1997)
              Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available royalty-free through LLMNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: -40ml3 fwd. ET from Amersham
              High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..36
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:1390119"
                /db_xref="taxon:9606"
                /clone="IMAGE:453763"
                /sex="male"
                /dev_stage="20 week-post conception fetus"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares fetal liver spleen INFLS S1"
                /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                This is a subtracted version of the original Soares fetal
                liver spleen INFLS library. 1st strand cDNA was primed
                with a Pac I - oligo(dT) primer [5',
                AACTGGAAGATATTAAGATCTTTTCTTTTCTTTT 3'].
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Pac I and cloned into the Pac I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M. Patricia Bonaldo."
ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 36;
Best Local Similarity 82.4%; Pred. No. 9.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CAGCTGGGACACAGAC 23
    |||||
Db 17 CAGCGGGGAAGAAGAC 1

RESULT 31
AJ239879
LOCUS          AJ239879
DEFINITION    Aspergillus niger ATCC6275 Aspergillus niger cDNA clone
              AN05D11, mRNA sequence.
ACCESSION     AJ239879
VERSION       AJ239879.1  GI:5443870
KEYWORDS      EST.
SOURCE        Aspergillus niger
ORGANISM      Aspergillus niger
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
              Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
              1 (bases 1 to 37)
REFERENCE     Choi, J.Y., Lee, D.W., Koh, J.S., Kim, J.H., Yang, M.S. and Chae, K.S.
AUTHORS       Identification of expressed sequence tags (ESTs) of the highly
TITLE
transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)
Contact: Chae KS
Faculty of Biological Sciences
Chonbuk National University
Chonju 561-756, Republic of Korea.
Location/Qualifiers
1..37
/organism="Aspergillus niger"
/mol_type="mRNA"
/strain="ATCC6275"
/db_xref="taxon:5061"
/clone="AN05D11"
/clone_lib="Aspergillus niger ATCC6275"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 37;
Best Local Similarity 77.8%; Pred. No. 9.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGACAA 20
    |||||
Db 20 TGCCCAACTGGGNAAAA 37

RESULT 32
AA287473
LOCUS          AA287473
DEFINITION    z850a12.r1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:700894 5.
              similar to dbj|D16558|SCJRDNA Scytosiphon lomentaria rDNA for 18S,
              5.8S and 25S (rRNA);, mRNA sequence.
ACCESSION     AA287473
VERSION       AA287473.1  GI:1933172
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@mail.nih.gov
              This clone is available royalty-free through LLMNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Trace considered overall poor quality
              Insert Length: 1111 Std Error: 0.00
              Seq primer: -28ml3 rev2 ET from Amersham
              High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..41
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:5740328"
                /db_xref="taxon:9606"
                /clone="IMAGE:700894"
                /tissue_type="germinal center B cell"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP GCBI"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was prepared from human tonsillar cells enriched for
                germinal center B cells by flow sorting (CD20+, IgD-),
                provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                primed with a Not I - oligo(dT) primer
                [5'-TGTTACCAATCTGAAGTGGAGCGCCGCTCATTTTCTTTT-3'
                ]. Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT7T3 vector. Library

```

went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 41;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAAGAC 23
||||| ||||| ||||| |||||
Db 3 CAGCAGGGAAGAAGAC 19

RESULT 33
AV957763 42 bp mRNA linear EST 14-MAR-2002
LOCUS AV957763 Nori Satoh unpublished cDNA library, egg Ciona
DEFINITION intestinalis cDNA clone cig05k15 5', mRNA sequence.
ACCESSION AV957763
VERSION AV957763.1 GI:19446062
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 42)
Sathoh.N., Satou.Y., Kohara.Y. and Shin-i.T.
Expressed genes in Ciona intestinalis

TITLE Unpublished (2000)
JOURNAL
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sathohascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers

FEATURES
source
1..42
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cig05k15"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 50.8%; Score 12.2; DB 1; Length 42;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
||||| ||||| ||||| |||||
Db 16 AGCTGTGGAAGAAGATG 32

RESULT 34
AU255694/c 44 bp mRNA linear EST 25-APR-2002
LOCUS AU255694 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BE00006185 3', mRNA sequence.
ACCESSION AU255694
VERSION AU255694.1 GI:20318679
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 44)
Kato,K. and Matoba,R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
JOURNAL

COMMENT

Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@bs.aist-nara.ac.jp, kkatob@bs.aist-nara.ac.jp/BED/index.html.
URL:http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

source
1..44
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0006185"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN

Query Match 50.8%; Score 12.2; DB 1; Length 44;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAAGAC 23
||||| ||||| ||||| |||||
Db 38 CAATTGGGAACAGGAC 22

RESULT 35

AJ792767

LOCUS

DEFINITION AJ792767 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.12.i08, mRNA sequence.

ACCESSION AJ792767

VERSION AJ792767.1 GI:51108095

KEYWORDS EST.

SOURCE Antirrhinum majus (snapdragon)

ORGANISM Antirrhinum majus

REFERENCE 1 (bases 1 to 45)

AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,

Saedler,H. and Zachgo,S.

TITLE Characterization of Antirrhinum Petal Development and

Identification of Target Genes of the Class B MADS Box Gene

DEFICIENS

JOURNAL Plant Cell 16 (12), 3197-3215 (2004)

PUBMED 15539471

COMMENT Contact: Schwarz-Sommer Z

Molekulare Pflanzen-genetik

MPI fuer Zuechtungs-forschung

Carl-von-Linne Weg 10, D-50829, Germany.

Location/Qualifiers

1..45

source

/organism="Antirrhinum majus"

/mol_type="mRNA"

/db_xref="taxon:4151"

/clone="018.2.12.i08"

/tissue_type="whole plant"

/clone_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 50.8%; Score 12.2; DB 1; Length 45;

Best Local Similarity 82.4%; Pred. No. 1e+06;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24

||||| ||||| ||||| |||||

Db 21 AGCTGCCGACACAGAG 37

RESULT 36

A1254367
 LOCUS qv33a10.x1 NCI_CGAP_Ov31 mRNA linear EST 03-FEB-1999
 DEFINITION similar to gb:U21696 cdai PROTHYMOSIN ALPHA (HUMAN); contains
 TARI.t1 TARI repetitive element ;, mRNA sequence.
 A1254367
 ACCESSION A1254367.1 GI:3861892
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 49)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuauqui,
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Insert Length: 307 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1983354"
 /sex="female"
 /tissue_type="papillary serous carcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ov31"
 /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian
 carcinoma, cDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 500 bp. Non-amplified library."
 ORIGIN
 Query Match 50.8%; Score 12.2; DB 1; Length 49;
 Best Local Similarity 82.4%; Pred. No. le+06; 3; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0
 QY 8 AGCTGGGGACACAGACG 24
 ||||||| |||||
 Db 10 AGGTGGGGAGGAAGACG 26
 RESULT 37
 A105506/c
 LOCUS A105506 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HRC12806, mRNA sequence.
 ACCESSION A105506.1 GI:13555027
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC12806"
 /clone_lib="Sugano Homo sapiens cDNA library"
 ORIGIN
 Query Match 50.8%; Score 12.2; DB 1; Length 50;
 Best Local Similarity 82.4%; Pred. No. le+06; 3; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0
 QY 1 GATCACACAGCTGGGGAA 17
 ||||| |||||
 Db 46 GCTGCTCACCCTGGGAA 30
 RESULT 38
 A105507/c
 LOCUS A105507 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HRC12884, mRNA sequence.
 ACCESSION A105507
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC12884"
 /clone_lib="Sugano Homo sapiens cDNA library"
 ORIGIN
 Query Match 50.8%; Score 12.2; DB 1; Length 50;
 Best Local Similarity 82.4%; Pred. No. le+06; 3; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0

Best Local Similarity 82.4%; Pred. No. 1e+06; Mismatches 3; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 1 GATGCACAGCTGGGAA 17
Db 46 GCTGCTCACCTGGGAA 30

RESULT 39
LOCUS C2909855 30 bp DNA linear GSS 08-AUG-2005
DEFINITION 4018011H10.1BL x1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.

ACCESSION C2909855
VERSION C2909855
KEYWORDS GSS.
SOURCE C2909855.1 GI:71923091

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 30)

AUTHORS

Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)

JOURNAL

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4018011 row: H column: 10

Class: transposon-tagged.

FEATURES

source

1..30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

/clone_lib="4018 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 50.0%; Score 12; DB 10; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAAACAGAC 23
Db 5 GCACAGATGGCGGCGAAAC 24

RESULT 40

DN955268

LOCUS

DEFINITION DN955268 33 bp mRNA linear EST 04-MAY-2005
it84h05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA sequence.

ACCESSION

DN955268.1 GI:63027406

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Gnetum gnemon

Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnepophyta; Gnepopsida; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 33)

AUTHORS

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Bali, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

TITLE

JOURNAL

COMMENT

FEATURES

source

1..33
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

ORIGIN

Query Match 50.0%; Score 12; DB 8; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGAAACAAG 21
Db 10 AAGCAAGCTGCGGCAAG 29

Search completed: December 13, 2005, 15:51:25
Job time : 2988 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 11:03:03 ; Search time 368.5 Seconds
(without alignments)
434.064 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatgcacagctggggaacaagacg 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	ADZ75766	Adz75766 Human ind
2	15.6	65.0	26	ADW69302	Adw69302 Forward p
C 3	15	62.5	38	AAQ74734	Aaq74734 KHCV enve
C 4	14.4	60.0	19	ADT77767	Adt77767 Livin RNA
C 5	14.4	60.0	20	AAD05966	Aad05966 Human dia
C 6	14.4	60.0	30	ABV76929	Abv76929 Blocking
C 7	14.4	60.0	42	ADF72069	Adf72069 Human XPC
C 8	14.2	59.2	21	ADS74065	Ads74065 Tumour su
C 9	14.2	59.2	22	ABZ30347	Abz30347 Candida a
C 10	14.2	59.2	23	AAx77148	Aax77148 Nerve mut
C 11	14.2	59.2	37	AAQ55126	Aaq55126 Primer fo
C 12	14.2	59.2	50	ABZ06705	Abz06705 Human leu
C 13	14.2	59.2	50	ABZ07095	Abz07095 Human leu
C 14	14	58.3	37	AAI47160	Aai47160 S pneumon
C 15	14	58.3	47	AAZ67650	Aaz67650 Human map
C 16	14	58.3	50	ABZ06403	Abz06403 Human leu
C 17	14	58.3	50	ABZ06793	Abz06793 Human leu
C 18	13.8	57.5	17	ABN08477	Abn08477 Human GDM
C 19	13.8	57.5	17	ACC52706	Acc52706 Human tum

ALIGNMENTS

RESULT 1

ID ADZ75766 standard; DNA; 24 BP.

AC ADZ75766;

DT 28-JUL-2005 (first entry)

DE Human inducible nitric oxide synthase gene exon 7 reverse PCR primer.
 XX ss; PCR; high altitude pulmonary edema; pulmonary edema;
 XX respiratory-gen.; respiratory disease; SNP detection; allelic variation;
 KW primer; exon.
 XX Homo sapiens.
 OS
 XX
 PN US2005106573-A1.
 XX
 PD 19-MAY-2005.
 XX
 PF 13-NOV-2003; 2003US-00713137.
 XX
 PR 13-NOV-2003; 2003US-00713137.
 XX (COUN-) COUNCIL SCI & IND RES INDIA.
 PA Pasha AQM, Ahsan A;
 XX
 DR WPI; 2005-384299/39.
 XX
 PT Detecting predisposition to high altitude pulmonary edema (HAPE) by
 PT amplifying intron 7 of human inducible nitric oxide synthase gene, and
 PT predicting and analyzing differences in the distribution of allelic
 variants.
 PS Claim 6; SEQ ID NO 3; 13pp; English.
 XX
 CC The invention relates to a novel method for detecting predisposition to
 CC high altitude pulmonary edema (HAPE). The method comprises amplifying
 CC intron 7 of the human inducible nitric oxide synthase (INOS) gene
 CC (ADZ75764) by designing and synthesizing forward and reverse
 CC oligonucleotide primers (ADZ75765+ADZ75766), and predicting and

20 13.8 57.5 17 13 ACN71567
 21 13.8 57.5 20 2 AAO53128
 C 22 13.8 57.5 20 2 AAT48684
 C 23 13.8 57.5 20 2 AAV20056
 24 13.8 57.5 20 2 AAV73038
 C 25 13.8 57.5 20 2 AAV73141
 26 13.8 57.5 20 6 ABL43554
 27 13.8 57.5 20 12 ADJ22962
 28 13.8 57.5 20 12 ADJ22962
 29 13.8 57.5 20 12 ADJ22961
 30 13.8 57.5 20 12 ADJ23531
 31 13.8 57.5 25 6 ABN13371
 32 13.8 57.5 25 6 ABN13372
 33 13.8 57.5 25 6 ABN13376
 34 13.8 57.5 25 6 ABN13373
 35 13.8 57.5 25 6 ABN13370
 36 13.8 57.5 25 6 ABN13377
 37 13.8 57.5 25 6 ABN13369
 38 13.8 57.5 25 6 ABN13374
 39 13.8 57.5 25 6 ABN13375
 C 40 13.8 57.5 25 12 ADQ80648
 41 13.8 57.5 25 13 ACN76465
 42 13.8 57.5 25 13 ACN76461
 43 13.8 57.5 25 13 ACN76463
 44 13.8 57.5 25 13 ACN76459
 45 13.8 57.5 25 13 ACN76467

Acn71567 Human GDM
 Aaq53128 Gene dete
 Aat48684 Probe for
 Aav20056 N-ras pro
 Aav73038 Human ras
 Aav73141 Human ras
 Aab143554 Human chr
 Adj22962 Human end
 Adj23298 Human end
 Adj22961 Human end
 Adj23531 Human end
 Abn13371 Human GDM
 Abn13372 Human GDM
 Abn13376 Human GDM
 Abn13373 Human GDM
 Abn13370 Human GDM
 Abn13377 Human GDM
 Abn13369 Human GDM
 Abn13374 Human GDM
 Abn13375 Human GDM
 Adq80648 Binding d
 Acn76465 Human GDM
 Acn76461 Human GDM
 Acn76463 Human GDM
 Acn76459 Human GDM
 Acn76467 Human GDM

CC statistically analyzing differences in the distribution of the allelic
 CC variants in the populations, where GG genotype at 19480 position are at
 CC low risk of HAPe, and AA genotype at 19480 position are at high risk of
 CC HAPe. The present sequence represents the forward oligonucleotide primer
 CC of the invention.

XX Sequence 24 BP; 8 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGAACAGACG 24
 |||||
 DB 1 GATGCACAGCTGGGAACAGACG 24

RESULT 2

ADW69302
 ID ADW69302 standard; DNA; 26 BP.

XX
 AC ADW69302;

DT 24-MAR-2005 (first entry)

XX Forward primer for PCR of chinese hamster beta-actin promoter.

DE
 XX Primer; ss; DNA amplification; PCR; beta-actin promoter.

XX
 KW Cricetulus griseus.

OS
 XX WO2005000888-A2.

PN
 XX 06-JAN-2005.

PD
 XX 24-JUN-2004; 2004WO-US017422.

PF
 XX 24-JUN-2003; 2003US-0480768P.

PR
 XX (GENZ) GENZYME CORP.

PA
 XX Estes SD, Zhang W;

PI
 XX WPI; 2005-058125/06.

XX New beta-actin and ribosomal protein S21 (rpS21) promoters, useful as
 PT enhancers and repressors for expression of heterologous nucleic acids
 PT encoding therapeutic proteins such as approximately alpha-glucosidase,
 PT antibodies, and insulin.

XX Example 2; SEQ ID NO 35; 95pp; English.

PS The present invention relates to new rodent beta-actin and ribosomal
 CC protein S21 (rpS21) promoters that have a low level of sequence homology
 CC to previously known B-actin and rpS21 promoters. The invention is based
 CC on the discovery that beta-actin promoters have higher promoter activity
 CC than CMV's promoter activity, and the discovery that the hamster rpS21
 CC promoter is at least as active as the hamster Beta-actin promoter when
 CC used for expressing certain genes. The nucleotide sequences are useful as
 CC probes for screening genomic libraries for isolation of genomic sequences
 CC that hybridize to one or more of the promoter sequences or their
 CC variants. The promoters are useful as enhancers and repressors, and in a
 CC vector for expression of heterologous nucleic acids encoding therapeutic
 CC proteins, such as alpha-glucosidase, acid sphingomyelinase, insulin,
 CC tissue plasminogen activator, thyrogen stimulating hormone,
 CC erythropoietin, glucocorticoidase, alpha-galactosidase and various
 CC antibodies. The present sequence is a forward primer for PCR detection of
 CC the chinese hamster beta-actin promoter containing intron 1.

XX Sequence 26 BP; 9 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 14; Length 26;
 Best Local Similarity 81.8%; Pred. No. 2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ATGCACAGCTGGGAACAGAC 23
 |||||
 DB 1 AGGCCACGCTTGGGACCAAGAC 22

RESULT 3

AAQ74734/c
 ID AAQ74734 standard; cDNA; 38 BP.

XX
 AC AAQ74734;

DT 25-MAR-2003 (revised)

DT 26-MAY-1995 (first entry)

XX KHCV envelope primer PE1EGT2.

XX Korean-type hepatitis C virus; KHCV; HCV; envelope protein; E1G; E2A;
 KW E2E; epitope; diagnosis; primer; polymerase chain reaction; PCR;
 KW amplification; ss.

XX Synthetic.

XX WO9425486-A1.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-KR000040.

XX 30-APR-1993; 93KR-00007440.

XX (LUCK-) LUCKY CO LTD.

XX Cho JM, Choi DY, Kim CH, So HS, Yang JY, Kim IS, Kim JH;

XX WPI; 1994-358190/44.

XX New Korean hepatitis C virus antigenic proteins - comprising epitopes of
 PT core protein, non-structural proteins or envelope protein, used for
 PT diagnosis.

XX Disclosure; Page 27; 91pp; English.

XX The primers given in AAQ74732-47 were used to amplify KHCV envelope gene
 CC fragments and to clone each fragment into a vector comprising the
 CC ubiquitin gene under control of the trp promoter, for expression in
 CC Escherichia coli W3110 (ATCC 37339), allowing identification of epitopes
 CC E1G (AAR62512), E2A (AAR62513) and E2E (AAR62514). Primer PE1EGT2
 CC comprises an Sali recognition site and nucleotides 1201-1221 of KHCV-
 CC LBC1. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 38 BP; 4 A; 12 C; 10 G; 12 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 2; Length 38;
 Best Local Similarity 78.3%; Pred. No. 3.9e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGAACAGAC 23
 |||||

DB 35 GGTGAACAGCTGGGAACACCAC 13
 |||||

RESULT 4

ADT77767/c
 ID ADT77767 standard; RNA; 19 BP.

XX
 AC ADT77767;

DT 30-DEC-2004 (first entry)

XX Livin RNA used to prepare siRNA for therapy-resistant tumour therapy.

KW Livin; inhibitor of apoptosis protein; short interfering RNA; siRNA;
KW RNAi; gene silencing; cytostatic; gene therapy; ss.
XX Homo sapiens.
XX
XX EP1469070-A1.
XX
XX 20-OCT-2004.
XX
XX 15-APR-2003; 2003EP-00008081.
XX
XX 15-APR-2003; 2003EP-00008081.
XX
XX (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.
XX
XX Butz K, Crnkovic-Mertens I, Hoppe-Seyler F;
XX WPI; 2004-730758/72.
XX
XX Use of a nucleic acid, or its fragment or derivative, for preparing livin
PT -specific siRNAs as an apoptosis inhibitor for the treatment of therapy-
PT resistant tumors.
XX
XX
XX Claim 1; SEQ ID NO 1; 22pp; English.
XX
XX The present sequence corresponds to nucleotides 611-629 of the coding
CC sequence of the livin (inhibitor of apoptosis protein) gene. Use of a
CC nucleic acid containing this sequence, or its fragment of derivative, to
CC prepare siRNA which sensitises therapy-resistant tumour cells for
CC apoptosis is claimed. The siRNA is preferably delivered into a therapy-
CC resistant tumour cell by using liposomes or hydrodynamic injection.
CC Another claimed nucleic acid AD77769 comprises DNA corresponding to the
CC present sequence joined, via a linker, to a complementary DNA strand.
CC This is also used to prepare siRNA which sensitises therapy-resistant
CC tumour cells for apoptosis, and is inserted into an expression vector
CC such as pSUPPER for production of double-stranded RNA. The siRNAs of the
CC invention are preferably used in combination with radiation therapy or
CC with a cytostatic compound, death receptor ligand, death receptor
CC antibody or negative regulator of anti-apoptotic proteins. The therapy
CC resistant tumour is neuroblastoma, intestinal carcinoma preferably
CC rectal, colon, familial adenomatous polyposis, hereditary non-polyposis
CC colorectal, oesophageal, labial, laryngeal, hypopharynx, salivary and
CC gastric carcinoma, adenocarcinoma, medullary thyroid carcinoma, papillary
CC thyroid carcinoma, follicular thyroid carcinoma, anaplastic thyroid
CC carcinoma, renal carcinoma, kidney parenchyma carcinoma, ovarian
CC carcinoma, cervical carcinoma, uterine carcinoma, endometrial carcinoma,
CC chorion carcinoma, pancreatic carcinoma, prostate carcinoma, testicular
CC carcinoma, breast carcinoma, urinary carcinoma, melanoma, brain tumours
CC preferably glioblastoma, astrocytoma, meningioma, medulloblastoma and
CC peripheral neuroectodermal tumours, Hodgkin's lymphoma, non-Hodgkin's
CC lymphoma, Burkitt's lymphoma, acute lymphatic leukaemia (ALL), chronic
CC lymphatic leukaemia (CLL), acute myeloid leukaemia (AML), chronic myeloid
CC leukaemia (CML), adult T-cell leukaemia lymphoma, hepatocellular
CC carcinoma, gall bladder carcinoma, bronchial carcinoma, small cell lung
CC carcinoma, non-small cell lung carcinoma, multiple myeloma, basaloma,
CC teratoma, retinoblastoma, choroida melanoma, seminoma, rhabdomyosarcoma,
CC craniopharyngioma, osteosarcoma, chondrosarcoma, myosarcoma, liposarcoma,
CC fibrosarcoma, Ewing sarcoma and plasmocytoma, and preferably cervical
CC carcinoma or melanoma (all claimed).
XX
SQ Sequence 19 BP; 2 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
Query Match 60.0%; Score 14.4; DB 13; Length 19;
Best Local Similarity 93.8%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 ACAGCTGGGGAACAG 21
DB 16 ACAGCTGGGGAACAG 1
RESULT 5
AAD05966/c

ID AAD05966 standard; DNA; 20 BP.
XX
XX AAD05966;
XX
XX 31-JUL-2001 (first entry)
XX
XX Human diacylglycerol kinase-zeta intron 22/exon 23 junction sequence.
XX
XX Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;
KW diacylglycerol kinase zeta; DGK; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH intron 1..10
FT /*tag= a
FT /number= 22
FT /partial
FT 11..20
FT /*tag= b
FT /number= 23
FT /partial
XX
XX US6221658-B1.
XX
XX 24-APR-2001.
XX
XX 25-AUG-1999; 99US-00382911.
XX
XX 22-APR-1996; 96US-0016210P.
XX 22-APR-1997; 97US-00841483.
XX (UTAH) UNIV UTAH RES FOUND.
XX
XX Prescott SM, Bunting M, Tang W, Topham M;
XX WPI; 2001-327248/34.
XX
XX New DNAs of the human diacylglycerol kinase, useful for modulating the
PT levels of diacylglycerol kinase in cells to catalyze the conversion of
PT diacylglycerol to phosphatidic acid, therefore increasing phosphatidic
PT acid levels.
XX
XX Disclosure; Col 17-18; 74pp; English.
XX
XX The patent discloses novel human diacylglycerol kinase (DGK) isoforms
CC namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta,
CC diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human
CC diacylglycerol kinase DNA is useful for coding human diacylglycerol
CC kinase, which is useful for catalysing the conversion of diacylglycerol
CC to phosphatidic acid. In particular, the human diacylglycerol kinase and
CC its DNA are useful for decreasing intracellular levels of diacyl-
CC glycerol (DAG) and for increasing intracellular levels of phosphatidic
CC acid in cells. The present DNA sequence is the exon/intron junction
CC sequence of human diacylglycerol kinase (DGK) zeta gene
XX
SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 60.0%; Score 14.4; DB 5; Length 20;
Best Local Similarity 93.8%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 GCACAGCTGGGGAACA 19
DB 16 GCACAGCTGGGGAACA 1
RESULT 6
ABV76929
ID ABV76929 standard; DNA; 30 BP.
XX
XX AC ABV76929;
XX

DT 03-MAR-2003 (first entry)
 XX
 DE Blocking oligonucleotide #5 for chymotrypsin B precursor.
 XX
 KW Nucleic acid synthesis; blocking agent; polymerase; DNA library;
 KW chymotrypsin B precursor; ss.
 XX
 OS Synthetic.
 XX
 XX EP1253205-A1.
 XX
 XX 30-OCT-2002.
 XX
 PF 24-APR-2001; 2001EP-00109971.
 XX
 PR 24-APR-2001; 2001EP-00109971.
 XX
 PA (LION-) LION BIOSCIENCE AG.
 XX
 XX Hoefler M, Kranz H, Klink M;
 PI WPI; 2003-077619/08.
 DR
 XX
 XX Preferential nucleic acid synthesis reaction of selected regions of
 PT target nucleic acids, by using a blocking agent which preferentially
 PT binds templates which are not desirable when amplifying the nucleic
 PT acids.
 XX
 XX Example 1; Page 6; 20pp; English.
 PS
 CC The specification describes a nucleic acid synthesis reaction of selected
 CC regions of target nucleic acids from a group of two different target
 CC nucleic acids. The method comprises combining in a reaction mixture, two
 CC different target nucleic acids, polymerase, additionally combining a
 CC blocking agent capable of binding a nucleic acid template molecule so
 CC that the polymerase is not able to utilize bound target nucleic acids as
 CC a template, and exposing the reaction mixture to a temperature at which
 CC nucleic acids are synthesized by the polymerase. The method is useful for
 CC nucleic acid synthesis reactions, and is especially useful for creating
 CC DNA libraries. ABV76929-30 represent blocking oligonucleotides, which are
 CC used in the method of the invention to block amplification of the
 CC chymotrypsin B precursor. The oligonucleotides are used to demonstrate
 CC the method of the invention
 XX
 XX Sequence 30 BP; 9 A; 2 C; 15 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 14.4; DB 8; Length 30;
 Best Local Similarity 75.0%; Pred. No. 7.3e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GATGCACAGCTGGGGACCAAGACG 24
 Db 6 GATGCACGGAGGGGGAGGAAGAGG 29
 RESULT 7
 ADF72069/c
 ID ADF72069 standard; DNA; 42 BP.
 XX
 AC ADF72069;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human XPC gene PCR primer SEQ ID NO:36.
 KW proliferation; cancer; cancer cell growth inhibition; human; PCR primer;
 KW ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003082078-A2.
 XX

PD 09-OCT-2003.
 XX
 PF 27-MAR-2003; 2003WO-US009428.
 XX
 PR 28-MAR-2002; 2002US-0368288P.
 PR 28-MAR-2002; 2002US-0368409P.
 XX
 PA (MEDI-) MEDICAL COLLEGE OHIO.
 XX
 XX Willey JC, Weaver DA, Warner KA, Graves TG, Demuth JP;
 PI Crawford EL;
 PI WPI; 2003-902899/82.
 DR
 XX
 XX Determining whether an agent can be used to reduce the proliferation,
 PT cause the death or inhibit the growth of cancer cell population by
 PT obtaining a sample of cancer cells and quantifying the level of
 PT expression of a marker in the cells.
 XX
 XX Example 1; SEQ ID NO 36; 106pp; English.
 PS
 CC The present invention describes a method for determining whether an agent
 CC can be used to reduce the proliferation and/or cause the death of cancer
 CC cells or inhibit the growth of a cancer cell population. The method is
 CC useful in determining whether an agent can be used to reduce the
 CC proliferation and/or cause the death of cancer cells or inhibit the
 CC growth of a cancer cell population. The present sequence represents a PCR
 CC primer which is used in the exemplification of the present invention.
 XX
 XX Sequence 42 BP; 4 A; 14 C; 6 G; 18 T; 0 U; 0 Other;
 SQ
 Query Match 60.0%; Score 14.4; DB 10; Length 42;
 Best Local Similarity 75.0%; Pred. No. 7.7e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GATGCACAGCTGGGGACCAAGACG 24
 Db 37 GATGAGAGGAGGGGACCAAGAG 14
 RESULT 8
 ADS74065
 ID ADS74065 standard; DNA; 21 BP.
 XX
 AC ADS74065;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Tumour suppressor p53 RT-PCR primer E11R.
 XX
 KW Tumour; suppressor; p53; splice variant; cytostatic; gene therapy;
 KW diagnosis; RT-PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1462521-A1.
 XX
 PD 29-SEP-2004.
 XX
 PF 27-MAR-2003; 2003EP-00007000.
 XX
 PR 27-MAR-2003; 2003EP-00007000.
 XX
 PA (DEPP/) DEPPERT W W.
 XX
 PI Deppert WW, Dornreiter I;
 PI WPI; 2004-663615/65.
 DR
 XX
 XX New nucleic acid encoding a p53 variant that can transactivate p21- and
 PT 14-3-3 sigma-promoter but not e.g. the p53-promoter, for obtaining
 PT complementary sequences capable of inhibiting expression of p53 variant
 PT and treating tumor.

XX Example 1; SEQ ID NO 17; 29pp; English.
 PS The present sequence is that of RT-PCR primer E11R for the p53 tumour
 CC suppressor gene. RT-PCR was used to detect possible alternative splicing
 CC of p53 in different primate cell lines. A novel isoform of p53 (deltap53)
 CC was identified that is generated by alternative exon splicing. RT-PCR
 CC showed that deltap53 lacks 198 nucleotides from exons 7, 8 and 9. The
 CC deletion junction contains a donor site-like splicing-cassette within the
 CC coding exon 7 (nucleotide 767) and an acceptor site-like splicing-
 CC cassette within the coding exon 9 (nucleotide 965). The resulting
 CC transcript contains a unique junction of exon 7 with 9, which does not
 CC alter the open reading frame. Thus, the novel p53-isoform lacks 66 amino
 CC acid residues from the central portion and hinge region of the protein
 CC but includes the functionally important C-terminal domain. The 984 bp
 CC transcript of deltap53 is found in human, African green monkey and Rhesus
 CC monkey. Unlike full-length p53, the p53 splice variant is capable of
 CC transactivating the endogenous p21- and 14-3-3sigma promoter but not the
 CC mdm2-, bax- or p103 promoter. The invention provides means for inhibiting
 CC the activity of the p53 variant, using antisense RNA or a ribozyme, for
 CC cancer therapy. Diagnostic compositions comprising a probe for detection
 CC of the splice variant are also claimed.

XX SQ Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 59.2%; Score 14.2; DB 13; Length 21;
 Best Local Similarity 84.2%; Pred. No. 8.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22
 ||||| ||||| |||||
 Db 1 GCTCAGTGGGGGAACAAGA 19

RESULT 9
 ABZ30347
 ID ABZ30347 standard; DNA; 22 BP.
 XX
 AC ABZ30347;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Candida albicans GRACE strain PCR primer SEQ ID NO 4498.
 XX
 KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
 XX
 OS Candida albicans.
 XX
 PN WO200253728-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US049486.
 XX
 PR 29-DEC-2000; 2000US-0259128P.
 PR 20-FEB-2001; 2001US-00792024.
 PR 22-AUG-2001; 2001US-0314050P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Roemer T, Jiang B, Boone C, Buessey H, Ohlsen KL;
 XX
 DR WPI; 2002-566694/60.
 XX
 PT Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele of
 PT a gene and placing other allele of the gene under conditional expression.
 XX
 PS Claim 36; SEQ ID NO 4498; 167pp + Sequence Listing; English.
 XX
 CC The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of a PCR
 CC primer used in the method of the invention. Note: The sequence data for
 CC this patent is not represented in the printed specification but is based
 CC on sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 22 BP; 6 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 59.2%; Score 14.2; DB 6; Length 22;
 Best Local Similarity 84.2%; Pred. No. 8.7e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGAACA 19
 ||||| ||||| |||||
 Db 4 GATGGAGAGCTGGTGAACA 22

RESULT 10
 AAX77148/c
 ID AAX77148 standard; DNA; 23 BP.
 XX
 AC AAX77148;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Nerve mutation factor DNA amplifying primer.
 XX
 KW Nerve mutation factor; chromosome 10; glioma; tumour suppressor;
 KW brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9925827-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 24-AUG-1998; 98WO-JP003737.
 XX
 PR 14-NOV-1997; 97JP-00313211.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Nakata M, Nakamura H, Yoshida M, Saya H;
 XX
 DR WPI; 1999-347474/29.
 XX
 PT Human gene on chromosome 10 homologous to Drosophila neuralized gene,
 PT useful in the diagnosis and gene therapy of brain tumors.
 XX
 PS Example; Page 25; 78pp; Japanese.
 XX
 CC The invention relates to a protein which is a nerve mutation factor and
 CC is the expression product of a gene located on chromosome 10. The gene is
 CC in a region frequently deleted in highly malignant gliomas. Sequences
 CC (AAX77135 and AAX77136) encoding human and mouse nerve mutation factors

DE XX
human leukocyte gene expression profiles in no

T7; leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;
rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
ss.

XX Homo sapiens.

XX WO200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US047856.

XX PR 20-OCT-2000; 2000US-0241994P.

XX PR 08-JUN-2001; 2001US-0296764P.

XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

XX PI Ly N, Woodward R, Quattermous T, Johnson F;

XX DR WPI; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or

XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis

XX PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX PS Claim 1; Page 556; Opp; English.

XX The invention relates to a system for detecting gene expression, which
comprises one or two isolated DNA molecules that detect expression of a
gene, where the gene corresponds to any of 8143 oligonucleotides
(ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful
for leukocyte expression profiling. It is particularly useful for
diagnosing a disease, monitoring (rate of) progression of a disease,
predicting therapeutic outcome, determining prognosis for a patient,
predicting disease complications in an individual or monitoring response
to treatment in an individual. The diseases include cardiac allograft
rejection, kidney allograft rejection, liver allograft rejection,
atherosclerosis, congestive heart failure, systemic lupus erythematosus,
rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

SQ Sequence 50 BP; 10 A; 15 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 6; Length 50;

Best Local Similarity 84.2%; Pred. No. 9.8e+03; Mismatches 3; Indels 0; Gaps 0;

XX Matches 16; Conservative 0;

QY 6 ACAGCTGGGACACAGACG 24

DB 49 ACAGCTGGAGACACAGAG 31

RESULT 14

AAAL47160

ID AAL47160 standard; DNA; 37 BP.

XX AC AAL47160;

XX DT 30-AUG-2002 (first entry)

XX DE S pneumoniae SpA gene PCR primer SH24.

XX KW SpA; pneumococcal; surface protein; secretory IgA; vaccine; infection;

XX KW PCR; primer; ss.

XX OS Streptococcus pneumoniae.

XX XX DE19708537-A1.

XX PD 10-SEP-1998.

XX PF 03-MAR-1997; 97DE-01008537.

XX 03-MAR-1997; 97DE-01008537.

XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX PI Chhatwal GS, Hammerschmidt S;

XX DR WPI; 1998-481924/42.

XX PT Pneumococcal surface protein SpA - for use in producing vaccines.

XX PS Example 6; Page 5-6; 12pp; German.

XX The present invention provides the protein and coding sequences of a
Streptococcus pneumoniae surface protein, called SpA, that binds to
secretory IgA. The sequences can be used in vaccines for treating
pneumococcal infections. The present sequence is a PCR primer used to
isolate the coding sequences of the invention

SQ Sequence 37 BP; 12 A; 10 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 37;

Best Local Similarity 77.3%; Pred. No. 1.2e+04; Mismatches 5; Indels 0; Gaps 0;

XX Matches 17; Conservative 0;

QY 1 GATGCACAGCTGGGGAACAAGA 22

DB 12 GATCCACAGCTGGGAACAAGA 33

RESULT 15

AAZ67650

ID AAZ67650 standard; DNA; 47 BP.

XX AC AAZ67650;

XX DT 10-SEP-2001 (first entry)

XX DE Human map-related biallelic marker SEQ ID NO:1997.

XX KW Human genome; biallelic marker; high density disequilibrium map;
genomic map; haplotype; phenotype; polymorphic base; genotyping;
haplotyping; hybridisation; identification; characterisation; diagnosis;
single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT variation replace(24,G)

XX FT /*tag= a

XX FT /standard_name= "single nucleotide polymorphism"

XX PN WO9954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-IB000822.

XX PR 21-APR-1998; 98US-0082614P.

XX PR 23-NOV-1998; 98US-0109732P.

XX PA (GEST) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.

XX PS Claim 1; Page 656; 2745pp; English.

XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 47 BP; 16 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 3; Length 47;
 Best Local Similarity 77.3%; Pred. No. 1.2e+04;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGAC 23
 ||||| |||||
 Db 25 ATGCACACCTGTTTCAAGAC 46

RESULT 16
 ABZ06403
 ID ABZ06403 standard; DNA; 50 BP.
 XX
 AC ABZ06403;
 XX
 DT 09-JAN-2003 (first entry)
 DE Human leukocyte gene expression profiling probe SEQ ID NO 6394.
 XX
 KW T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200257414-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-OCT-2001; 2001WO-US047856.
 XX
 PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX
 PA (BIOC-) BIOCARDIA INC.
 XX
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 XX WPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 536; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 XX
 PS Claim 1; Page 536; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response

CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 16 A; 8 C; 19 G; 7 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GCTGGGGGAACAAGA 22
 ||||| |||||
 Db 31 GCTGGGGGAACAAGA 44

RESULT 17
 ABZ06793/c
 ID ABZ06793 standard; DNA; 50 BP.
 XX
 AC ABZ06793;
 XX
 DT 09-JAN-2003 (first entry)
 DE Human leukocyte gene expression profiling probe SEQ ID NO 6784.
 XX
 KW T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200257414-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 22-OCT-2001; 2001WO-US047856.
 XX
 PR 20-OCT-2000; 2000US-0241994P.
 PR 08-JUN-2001; 2001US-0296764P.
 XX
 PA (BIOC-) BIOCARDIA INC.
 XX
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quertermous T, Johnson F;
 XX
 XX WPI; 2002-636525/68.
 XX
 PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 547; Opp; English.
 XX
 CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX
 SQ Sequence 50 BP; 7 A; 19 C; 8 G; 16 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 GCTGGGGAACAAGA 22
Db 20 GCTGGGGAACAAGA 7

RESULT 18
ABN08477
ID ABN08477 standard; DNA; 17 BP.
AC ABN08477;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8469.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207458P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000682.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8469; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
SQ

Query Match 57.5%; Score 13.8; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 AGCTGGGGAACAAGACG 24
Db 1 AGCTGGGGAACAATGACG 17

RESULT 19
ACC52706/c
ID ACC52706 standard; DNA; 17 BP.
XX
XX ACC52706;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #1473.
XX
XX ss: tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX
XX FR2826373-A1.
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
PF
XX 20-JUN-2001; 2001FR-00008139.
PR
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijnder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 380; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 0 Other;
SQ

Query Match 57.5%; Score 13.8; DB 10; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 ATGCACAGCTGGGGAC 18
Db 17 ATGCACAGCTGGGGATC 1

RESULT 20

ACN71567
 ID ACN71567 standard; DNA; 17 BP.
 XX
 AC ACN71567;
 XX
 XX 02-DEC-2004 (first entry)
 XX
 XX Human GDMPLP-1 probe SEQ ID NO:8469.
 DE
 XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 XX Homo sapiens.
 OS
 XX US2004137589-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 26-NOV-2003; 2003US-00723361.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000SB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 XX (GUIYY/) GU Y.
 PA (JIYY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 DR
 XX
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 PT
 XX
 XX Disclosure; SEQ ID NO 8469; 0pp; English.
 PS
 XX
 XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 13; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 6 ACAGCTGGGGAACAAGA 22
 DB 1 ACAGCTGGGGAACAAGA 17
 RESULT 22
 AAT48684/c
 ID AAT48684 standard; DNA; 20 BP.
 XX
 AC AAT48684;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-OCT-1997 (first entry)
 DT
 XX
 DE Probe for detecting N-ras gene mutations in the codon at position 61.
 KW Mutated codon; single base mutation; human; acute myeloid leukaemia;
 KW tumour; activated ras gene; N-ras; H-ras; K-ras; ss.

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 AGCTGGGGAACAAGACG 24
 DB 1 AGCTGGGGAACAAGACG 17
 RESULT 21
 AAQ53128
 ID AAQ53128 standard; DNA; 20 BP.
 XX
 AC AAQ53128;
 XX
 XX 03-JUN-1994 (first entry)
 DT
 XX Gene detection sequence 52.
 DE
 XX Gene detection; radio-isotopes; target gene; electrode; detection;
 KW optical fibre; hybridise; hybridisation; electrochemical; photochemical;
 KW electrolysis; probe; ss.
 KW
 XX Synthetic.
 OS
 XX JP05285000-A.
 PN
 XX 02-NOV-1993.
 PD
 XX 10-SEP-1992; 92JP-00242397.
 PF
 XX 13-FEB-1992; 92JP-00025621.
 PR
 XX (TOKE) TOSHIBA KK.
 PA
 XX WPI; 1993-382240/48.
 DR
 XX
 XX Detection method of gene without using radio-isotope - by hybridisation
 PT of nucleic acid probe which is single strand having complementary
 PT sequence of gene and single strand denatured sample DNA.
 PT
 XX Disclosure; Page 23; 26pp; Japanese.
 PS
 XX The sequences (AAQ53077-Q53136) are used in the invention to detect
 CC specific genes without the use of radio-isotopes. Detection is carried
 CC out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic
 CC acid probe, complementary to the target sequence. Hybridisation occurs on
 CC the surface of an electrode or optical fibre and detection is visualised
 CC by the addition of an entity that recognises (ds) hybridised DNA and is
 CC electrochemically / photochemically active
 CC
 XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 57.5%; Score 13.8; DB 2; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 ACAGCTGGGGAACAAGA 22
 DB 1 ACAGCTGGGGAACAAGA 17
 RESULT 22
 AAT48684/c
 ID AAT48684 standard; DNA; 20 BP.
 XX
 AC AAT48684;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-OCT-1997 (first entry)
 DT
 XX
 DE Probe for detecting N-ras gene mutations in the codon at position 61.
 KW Mutated codon; single base mutation; human; acute myeloid leukaemia;
 KW tumour; activated ras gene; N-ras; H-ras; K-ras; ss.

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XX OS Synthetic.
XX PN US5591582-A.
XX PD 07-JAN-1997.
XX PF 23-JUN-1994; 9AUS-00264425.
XX PR 23-JUL-1985; 85US-00758104.
XX PR 04-AUG-1987; 87US-00081490.
XX PR 21-APR-1992; 92US-00873352.
XX XX (UYLE-) RIJKSUNIV LEIDEN.
XX PN Van Der Eb AJ, Bos JL;
XX PI WPI; 1997-086629/08.
XX DR
XX PT Detection of activated ras gene - using oligo:nucleotide probes to detect
XX PT mutated codon.
XX PS Claim 25; Col 29; 20pp; English.
XX CC A new method has been produced for the detection of an activated ras gene
XX CC containing a mutated codon. The method involves: either cleaving a human
XX CC subject's genomic DNA with a restriction enzyme to produce DNA fragments
XX CC and treating the fragments to obtain single-stranded DNA molecules or
XX CC isolating the subject's polyA+ mRNA; contacting the single-stranded DNA
XX CC molecules or polyA+ mRNA under hybridising conditions with a labelled
XX CC synthetic DNA molecule, optionally bound to a solid support, comprising
XX CC 12-20 nucleotides, where the synthetic DNA molecule is 5'-B-Q-D-3', in the
XX CC case of single-stranded DNA or is complementary to 5'-B-Q-D-3', in the
XX CC case of polyA+ mRNA, B = 0-9 nucleotides having a sequence complementary
XX CC to a sequence in the activated ras gene 5' of the mutated codon, D = 0-12
XX CC nucleotides having a sequence complementary to a sequence in the
XX CC activated ras gene 3' of the mutated codon, provided that B and D contain
XX CC a total of at least 9 nucleotides, and Q is complementary to the mutated
XX CC codon; treating the resulting hybridised molecules under conditions
XX CC permitting only fully complementary molecules to remain hybridised; and
XX CC detecting the presence of the labelled synthetic DNA molecule in the
XX CC hybridised molecules. The present sequence represents the synthetic DNA
XX CC probe used for detecting the activated N-ras gene when the mutated codon
XX CC is at position 61 and has a single base substitution in the first or
XX CC second nucleotide position so that it encodes an amino acid other than
XX CC Glu. The method can be used for the diagnosis of acute myeloid leukaemia
XX CC and other tumours. (Updated on 25-MAR-2003 to correct PF field.)
XX XX
XX SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGACACAGA 22
Db 20 ACAGCTGGAGAGAAGA 4

RESULT 23
AAV20056/c
ID AAV20056 standard; DNA; 20 BP.
XX AC AAV20056;
XX DT 06-JUL-1998 (first entry)
XX DE N-ras probe 665T.
XX KW Probe; N-ras; mutation detection; mismatch binding protein;
XX KW cancer diagnosis; single strand binding protein; ss.
XX OS Synthetic.

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XX PN WO9745555-A1.
XX PD 04-DEC-1997.
XX PF 22-MAY-1997; 97WO-SB000839.
XX PR 29-MAY-1996; 96SE-00002062.
XX XX (PHAA ) PHARMACIA BIOTECH AB.
XX PN Hasebe M, Goto M, Tosu M;
XX DR WPI; 1998-130209/12.
XX PT Method for detecting mutation(s) by mismatch binding protein - useful for
XX PT separating mutation from non-mutated target polynucleotide in sample,
XX PT used in early diagnosis of cancer.
XX PS Disclosure; Page 9; 24pp; English.
XX CC This sequence represents a probe for the N-ras gene, that can be used in
XX CC the method of the invention. The method is for detecting a mutation
XX CC from a non-mutated sequence of a target polynucleotide (TP) in a sample,
XX CC by using a mismatch binding protein (MBP), comprises: (a) providing a non
XX CC -mutated and mutated TP; (b) forming duplex of the non-mutated and
XX CC mutated single strands of TP in (a); (c) adding a single strand binding
XX CC protein to the polynucleotide from (b); (d) incubating MBP with an
XX CC activating agent; (e) adding the incubated MBP from (d) to the
XX CC polynucleotide from (c), so that MBP binds to the duplex formed by one
XX CC non-mutated and one mutated single strand of TP; and (f) detecting the
XX CC presence of any MBP bound to TP. The method may be used for early
XX CC diagnosis of cancer. Binding of MBP to single strands is inhibited by the
XX CC single strand binding protein. By activating MBP with an activator,
XX CC before addition to the sample, binding to double strands lacking
XX CC mismatches does not take place
XX SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGACACAGA 22
Db 20 ACAGCTGGAGAGAAGA 4

RESULT 24
AAV73038
ID AAV73038 standard; DNA; 20 BP.
XX AC AAV73038;
XX DT 09-FEB-1999 (first entry)
XX DE Human ras oncogene probe #13.
XX KW Ras oncogene; probe; point mutation; detection; cancer; ss.
XX OS Synthetic.
XX PN US5847095-A.
XX DR 08-DEC-1998.
XX PF 03-JAN-1997; 97US-00778543.
XX PR 23-JUL-1985; 85US-00758104.
XX PR 04-AUG-1987; 87US-00081490.
XX PR 21-APR-1992; 92US-00873352.
XX PR 23-JUN-1994; 94US-00264425.
XX OS

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PA (UYLE-) RIJKSUNIV LEIDEN.
 XX Bos JL, Van Der Eb AJ;
 XX WPI; 1999-059149/05.
 DR Probes for detecting ras oncogene point mutations - useful for the
 XX diagnosis of cancer associated with single base mutations.
 PT Claim 6; Col 5; 18pp; English.
 XX
 XX AAV73026-V73071 are probes used to detect a single-base mutation in a
 CC human ras oncogene. These probes comprise 12-43 nucleotides of formula 5'
 CC -B-Q-D-3', Q = 3 nucleotides complementary to the mutated codon, and B
 CC and D each = 0-20 nucleotides complementary to the ras sequences flanking
 CC the mutated codon. The probes are useful for detecting cancers associated
 CC with point mutations
 XX
 XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 57.5%; Score 13.8; DB 2; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX

QY 6 ACAGCTGGGGAACAAGA 22
 ||||| |||||
 DB 1 ACAGCTGGGGAAGAAGA 17

RESULT 25
 AAV73141/c
 ID AAV73141 standard; DNA; 20 BP.
 XX
 AC AAV73141;
 XX
 DT 09-FEB-1999 (first entry)
 XX
 DE Human ras oncogene mutant detecting oligomer N-61a.
 XX
 KW Ras oncogene; probe; point mutation; detection; cancer; ss.
 XX
 OS Synthetic.
 XX
 PN US5847095-A.
 XX
 PD 08-DEC-1998.
 XX
 PF 03-JAN-1997; 97US-00778543.
 XX
 PR 23-JUL-1985; 85US-00758104.
 XX
 PR 04-AUG-1987; 87US-00081490.
 XX
 PR 21-APR-1992; 92US-00873352.
 XX
 PR 23-JUN-1994; 94US-00264425.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Bos JL, Van Der Eb AJ;
 XX WPI; 1999-059149/05.
 DR Probes for detecting ras oncogene point mutations - useful for the
 XX diagnosis of cancer associated with single base mutations.
 PT Disclosure; Col 19-20; 18pp; English.
 XX
 XX AAV73084-V73145 are oligomers used in a method to detect a single-base
 CC mutation in a human ras oncogene. These probes comprise 12-43 nucleotides
 CC of formula 5'-B-Q-D-3', Q = 3 nucleotides complementary to the mutated
 CC codon, and B and D each = 0-20 nucleotides complementary to the ras
 CC sequences flanking the mutated codon. The probes are useful for detecting
 CC cancers associated with point mutations
 XX
 XX Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 ACAGCTGGGGAACAAGA 22
 ||||| |||||
 DB 20 ACAGCTGGGGAAGAAGA 4

RESULT 26
 ABL43554
 ID ABL43554 standard; DNA; 20 BP.
 XX
 AC ABL43554;
 XX
 DT 11-APR-2002 (first entry)
 XX
 DE Human chromosome 1p36-35 PCR primer SEQ ID NO:598.
 XX
 KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001321190-A.
 XX
 PD 20-NOV-2001.
 XX
 PF 12-MAR-2001; 2001JP-00068285.
 XX
 PR 10-MAR-2000; 2000JP-00066716.
 XX
 PA (RIKA) RIKAKAKU KENKYUSHO.
 PA (GENO-) GENOTEX YG.
 XX
 DR WPI; 2002-144136/19.
 XX
 PT Arraying genome clones.
 XX
 PS Claim 4; Page 16; 528pp; Japanese.
 XX

The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 7 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
 XX

Query Match 57.5%; Score 13.8; DB 6; Length 20;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 AGCTGGGGAACAAGACG 24
 ||||| |||||
 DB 4 AGCTGGTGAAGAAGACG 20

```

RESULT 27
ADJ22962
ID ADJ22962 standard; DNA; 20 BP.
XX
XX AC ADJ22962;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1360.
XX
XX KW Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
XX KW cardiovascular disorder; metabolic syndrome X; ss.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "This oligonucleotide has a phosphorothioate
XX backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
XX and 3' ends, which are 4 nucleotides in length. Also all
XX cytidine residues are 5-methylcytidines"
XX
XX PN WO2004009541-A2.
XX
XX XX 29-JAN-2004.
XX
XX PF 18-JUL-2003; 2003WO-US022410.
XX
XX PR 19-JUL-2002; 2002US-0397106P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Bhat BG;
XX
XX DR WPI; 2004-132912/13.
XX
XX PT New antisense oligonucleotide for modulating endothelial lipase
XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX
XX PS Claim 3; SEQ ID NO 1360; 1007pp; English.
XX
XX CC The present invention relates to antisense oligonucleotides (ADJ21603-
XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX SQ Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 57.5%; Score 13.8; DB 12; Length 20;
XX Best Local Similarity 88.2%; Pred. No. 1.3e+04;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
Db 4 AGCTGGGGAACAAGACG 20

RESULT 28
ADJ23298
ID ADJ23298 standard; DNA; 20 BP.
XX

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AC ADJ23298;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1696.
XX
XX KW Antilipemic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
XX Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
XX KW cardiovascular disorder; metabolic syndrome X; ss.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "This oligonucleotide has a phosphorothioate
XX backbone and 2'-methoxyethyl (2'-MOE) wings at the 5',
XX and 3' ends, which are 4 nucleotides in length. Also all
XX cytidine residues are 5-methylcytidines"
XX
XX PN WO2004009541-A2.
XX
XX XX 29-JAN-2004.
XX
XX PF 18-JUL-2003; 2003WO-US022410.
XX
XX PR 19-JUL-2002; 2002US-0397106P.
XX
XX PA (PHAA ) PHARMACIA CORP.
XX
XX PI Bhat BG;
XX
XX DR WPI; 2004-132912/13.
XX
XX PT New antisense oligonucleotide for modulating endothelial lipase
XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX PT high density lipoprotein or cardiovascular disorders.
XX
XX PS Claim 3; SEQ ID NO 1696; 1007pp; English.
XX
XX CC The present invention relates to antisense oligonucleotides (ADJ21603-
XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX CC (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX CC with and inhibits the expression of EL. The antisense oligonucleotides
XX CC are useful for modulating the expression of endothelial lipase in cells
XX CC or tissues to treat diseases associated with EL expression, such as
XX CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX CC disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX CC used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 57.5%; Score 13.8; DB 12; Length 20;
XX Best Local Similarity 88.2%; Pred. No. 1.3e+04;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
Db 1 AGCTGGGGAACAAGACG 17

RESULT 29
ADJ22961
ID ADJ22961 standard; DNA; 20 BP.
XX
XX AC ADJ22961;
XX
XX XX 20-MAY-2004 (first entry)
XX
XX DE Human endothelial lipase antisense oligonucleotide, SEQ ID 1359.
XX

```

```

KW Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "This oligonucleotide has a phosphorothioate
FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT and 3' ends, which are 4 nucleotides in length. Also all
FT cytidine residues are 5-methylcytidines"
XX
PN WO2004009541-A2.
XX
XX 29-JAN-2004.
XX
XX 18-JUL-2003; 2003WO-US022410.
XX
XX 19-JUL-2002; 2002US-0397106P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Bhat BG;
XX
XX WPI; 2004-132912/13.
XX
XX New antisense oligonucleotide for modulating endothelial lipase
XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX high density lipoprotein or cardiovascular disorders.
XX
XX Claim 3; SEQ ID NO 1359; 1007pp; English.
XX
XX The present invention relates to antisense oligonucleotides (ADJ21603-
XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX with and inhibits the expression of EL. The antisense oligonucleotides
XX are useful for modulating the expression of endothelial lipase in cells
XX or tissues to treat diseases associated with EL expression, such as
XX dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;
XX
Query Match 57.5%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
Db ||||| ||||| |||||
3 AGCTGGGGAACAAGACG 19

RESULT 30
ADJ23531
ID ADJ23531 standard; DNA; 20 BP.
XX
XX ADJ23531;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human endothelial lipase antisense oligonucleotide, SEQ ID 1929.
XX
XX Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;
KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;
KW cardiovascular disorder; metabolic syndrome X; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "This oligonucleotide has a phosphorothioate
XX backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
XX and 3' ends, which are 4 nucleotides in length. Also all
XX cytidine residues are 5-methylcytidines"
XX
XX WO2004009541-A2.
XX
XX 29-JAN-2004.
XX
XX 18-JUL-2003; 2003WO-US022410.
XX
XX 19-JUL-2002; 2002US-0397106P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Bhat BG;
XX
XX WPI; 2004-132912/13.
XX
XX New antisense oligonucleotide for modulating endothelial lipase
XX expression, for diagnosing, preventing or treating e.g. dyslipidemia, low
XX high density lipoprotein or cardiovascular disorders.
XX
XX Claim 3; SEQ ID NO 1929; 1007pp; English.
XX
XX The present invention relates to antisense oligonucleotides (ADJ21603-
XX ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence
XX (ADJ25517), where the antisense oligonucleotide specifically hybridises
XX with and inhibits the expression of EL. The antisense oligonucleotides
XX are useful for modulating the expression of endothelial lipase in cells
XX or tissues to treat diseases associated with EL expression, such as
XX dyslipidaemia, low high density lipoprotein (HDL), cardiovascular
XX disorder or metabolic syndrome X. In addition, the oligonucleotides are
XX used for diagnostics, prophylaxis, or as research reagents or kits.
XX
XX Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
XX
Query Match 57.5%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
Db ||||| ||||| |||||
2 AGCTGGGGAACAAGACG 18

RESULT 31
ABN13371
ID ABN13371 standard; DNA; 25 BP.
XX
XX ABN13371;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13363.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX

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PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 XX WPI; 2002-179446/23.
 DR
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 PT
 XX
 XX Disclosure; SEQ ID NO 13363; 214pp; English.
 PS
 XX
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 57.5%; Score 13.8; DB 6; Length 25;
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 AGCTGGGGAACAAGACG 24
 DB 7 AGCTGGAGAACATGACG 23
 RESULT 32
 ABN13372
 ID ABN13372 standard; DNA; 25 BP.
 XX
 AC ABN13372;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13364.
 DE
 XX Human; genome-derived myosin-like protein 1; hGDMLP-1; heart;
 KW

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI
 XX WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 PT
 XX
 XX Disclosure; SEQ ID NO 13364; 214pp; English.
 PS
 XX
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 7 A; 6 C; 10 G; 2 T; 0 U; 0 Other;
 Query Match 57.5%; Score 13.8; DB 6; Length 25;
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 AGCTGGGGAACAAGACG 24
 DB 6 AGCTGGAGAACATGACG 22

RESULT 33
ABN13376
ID ABN13376 standard; DNA; 25 BP.
XX AC ABN13376;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13368.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;
XX WPI; 2002-179446/23.
XX DR
XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX PS Disclosure; SEQ ID NO 13368; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequence

SQ Sequence 25 BP; 9 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
DB 2 AGCTGGAGAACATGACG 18
RESULT 34
ABN13373
ID ABN13373 standard; DNA; 25 BP.
XX AC ABN13373;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13365.
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;
XX WPI; 2002-179446/23.
XX DR
XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX PS Disclosure; SEQ ID NO 13365; 214pp; English.
XX CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX
 SQ Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.4e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 AGCTGGGGAACAGACG 24

Db 5 AGCTGGGGAACATGACG 21

RESULT 35

ABN13370

ID ABN13370 standard; DNA; 25 BP.

XX

AC ABN13370;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13362.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PR 30-JAN-2001; 2001WO-US000661.

XX

PR 30-JAN-2001; 2001WO-US000662.

XX

PR 30-JAN-2001; 2001WO-US000663.

XX

PR 30-JAN-2001; 2001WO-US000664.

XX

PR 30-JAN-2001; 2001WO-US000665.

XX

PR 30-JAN-2001; 2001WO-US000666.

XX

PR 30-JAN-2001; 2001WO-US000667.

XX

PR 30-JAN-2001; 2001WO-US000668.

XX

PR 30-JAN-2001; 2001WO-US000669.

XX

PR 30-JAN-2001; 2001WO-US000670.

XX

PR 05-FEB-2001; 2001US-0266860P.

XX

XX (AEOM-) AEOMICA INC.

XX

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

SQ Sequence 25 BP; 8 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.4e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 AGCTGGGGAACAGACG 24

Db 8 AGCTGGGGAACATGACG 24

RESULT 36

ABN13377

ID ABN13377 standard; DNA; 25 BP.

XX

AC ABN13377;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13369.

XX

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WO200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PR 30-JAN-2001; 2001WO-US000661.

XX

PR 30-JAN-2001; 2001WO-US000662.

XX

PR 30-JAN-2001; 2001WO-US000663.

XX

PR 30-JAN-2001; 2001WO-US000664.

XX

PR 30-JAN-2001; 2001WO-US000665.

XX

PR 30-JAN-2001; 2001WO-US000666.

XX

PR 30-JAN-2001; 2001WO-US000667.

XX

PR 30-JAN-2001; 2001WO-US000668.

XX

PR 30-JAN-2001; 2001WO-US000669.

XX

PR 30-JAN-2001; 2001WO-US000670.

XX

PR 05-FEB-2001; 2001US-0266860P.

XX

XX (AEOM-) AEOMICA INC.

XX

XX
 SQ Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
 Query Match 57.5%; Score 13.8; DB 6; Length 25;
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 8 AGCTGGGGAACAGACG 24
 Db 5 AGCTGGGGAACATGACG 21
 RESULT 35
 ABN13370
 ID ABN13370 standard; DNA; 25 BP.
 XX
 AC ABN13370;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13362.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PR 30-JAN-2001; 2001WO-US000661.
 XX
 PR 30-JAN-2001; 2001WO-US000662.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 XX
 PR 30-JAN-2001; 2001WO-US000664.
 XX
 PR 30-JAN-2001; 2001WO-US000665.
 XX
 PR 30-JAN-2001; 2001WO-US000666.
 XX
 PR 30-JAN-2001; 2001WO-US000667.
 XX
 PR 30-JAN-2001; 2001WO-US000668.
 XX
 PR 30-JAN-2001; 2001WO-US000669.
 XX
 PR 30-JAN-2001; 2001WO-US000670.
 XX
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 13362; 214pp; English.
 XX
 XX The present invention describes a human genome-derived myosin-like

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 13369; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 10 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAGACG 24
DB 1 AGCTGGGGAACATGACG 17

RESULT 37
ABN13369
ID ABN13369 standard; DNA; 25 BP.
XX
XX ABN13369;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13361.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234587P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 13361; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAGACG 24
DB 9 AGCTGGGGAACATGACG 25

RESULT 38
ABN13374
ID ABN13374 standard; DNA; 25 BP.
XX
XX ABN13374;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13366.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX

PD 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
PA Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 13366; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
SQ Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
DB 4 AGCTGGGGAACAATGACG 20
RESULT 39
ABN13375
ID ABN13375 standard; DNA; 25 BP.
XX
AC ABN13375;
XX
DT 29-MAY-2002 (first entry)

XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13367.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 13367; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24

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Db      ||||| ||||| |||||
3 ACCTGGAGAACATGACG 19

RESULT 40
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ID ADQ80648 standard; DNA; 25 BP.
XX
AC ADQ80648;
XX
DT 09-SEP-2004 (first entry)
XX
DE Binding domain-functional group fusion related pRK primer.
XX
KW dimer; chimeric recombinant binding domain-functional group fusion;
KW steric hindrance; PCR; primer; ss.
XX
OS Unidentified.
XX
PN KR2004004095-A.
XX
PD 13-JAN-2004.
XX
PF 30-JUN-2003; 2003KR-00043599.
XX
PR 29-JUN-2002; 2002KR-00037770.
XX
PA (CHOE/) CHO E M H.
XX
PI Choe MH, Choi SH, Kim YJ, Kwon HW, Lee YC, Song JH, Won JS;
PI Yoo MH;
XX
DR WPI; 2004-370653/35.
XX
PT Dimer of chimeric recombinant binding domain-functional group fusion
PT formed via disulfide-bond-bridge and production process thereof.
XX
PS Example 3; Page 25; 65pp; Korean.
XX
XX The invention describes a dimer of a chimeric recombinant binding domain-
XX functional group fusion formed via disulfide-bond-bridge and a production
XX process thereof. The dimer has two times-improved adhesion, and
XX excellently functions on a target. A dimer of chimeric recombinant
XX binding domain-functional group fusion is provided, wherein an extended
XX amino acid sequence (Ext) which is extended from the binding domain (B)
XX to the function group (F) fuses the binding domain (B) and the functional
XX group (F); the extended amino acid sequence (Ext) contains cysteine
XX without an inner chain pair and forms disulfide-bond-bridge when the
XX cysteine is oxidised; and a flexible amino acid sequence (Flx) is
XX contained between the last cysteine and the functional group (F), and
XX consists of flexible amino acid sequences of GASQEND, so that it can
XX decrease steric hindrance between the functional group when the chimeric
XX recombinant binding domain(B)-functional group (F) fusion forms the
XX dimer. This sequence represents a primer associated with the chimeric
XX recombinant binding domain-functional group fusion of the invention.
XX
SQ Sequence 25 BP; 1 A; 10 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCACAGCTGGGGAACAA 20
||| ||||| |||||
Db 17 GCGGCGCTGGGGAACAA 1
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OM nucleic - nucleic search, using sw model
Run on: December 13, 2005, 12:48:14 ; Search time 1116.5 Seconds
(without alignments)
1221.892 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatgcacagctggggaacaagacg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_ats.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15.6	65.0	26	6	CQ979281	Sequence
C 3	15	62.5	38	6	AR071012	Sequence
4	14.6	60.8	47	6	AR290262	Sequence
C 5	14.4	60.0	19	6	CQ890345	Sequence
C 6	14.4	60.0	19	6	CQ896981	Sequence
7	14.4	60.0	30	6	AX588101	Sequence
8	14.4	60.0	30	6	AX642888	Sequence
9	14.2	59.2	21	6	CQ878645	Sequence
10	14.2	59.2	22	6	CQ890107	Sequence
11	14.2	59.2	22	6	AX487198	Sequence
C 12	14.2	59.2	23	6	E26387	Neuralized
13	14	58.3	37	6	A86551	Sequence 13
14	14	58.3	37	6	BD082235	Surface p
15	14	58.3	47	6	AR290163	Sequence
16	13.8	57.5	17	6	CQ623729	Sequence
17	13.8	57.5	17	6	AR464792	Sequence
C 18	13.8	57.5	17	6	AX673028	Sequence

C	19	13.8	57.5	20	6	AR167144	Sequence
	20	13.8	57.5	20	6	BD088354	A method
	21	13.8	57.5	20	6	I02471	Sequence 3
	22	13.8	57.5	20	11	AB067911	Synthetic
	23	13.8	57.5	25	6	CQ628621	Sequence
	24	13.8	57.5	25	6	CQ628622	Sequence
	25	13.8	57.5	25	6	CQ628623	Sequence
	26	13.8	57.5	25	6	CQ628624	Sequence
	27	13.8	57.5	25	6	CQ628625	Sequence
	28	13.8	57.5	25	6	CQ628626	Sequence
	29	13.8	57.5	25	6	CQ628627	Sequence
	30	13.8	57.5	25	6	CQ628628	Sequence
	31	13.8	57.5	25	6	CQ628629	Sequence
	32	13.8	57.5	25	6	AR469684	Sequence
	33	13.8	57.5	25	6	AR469685	Sequence
	34	13.8	57.5	25	6	AR469686	Sequence
	35	13.8	57.5	25	6	AR469687	Sequence
	36	13.8	57.5	25	6	AR469688	Sequence
	37	13.8	57.5	25	6	AR469689	Sequence
	38	13.8	57.5	25	6	AR469690	Sequence
	39	13.8	57.5	25	6	AR469691	Sequence
	40	13.8	57.5	25	6	AR469692	Sequence
	41	13.8	57.5	29	6	BD082096	Reagents
C	42	13.8	57.5	42	6	AX734289	Sequence
C	43	13.8	57.5	47	6	AR292118	Sequence
C	44	13.6	56.7	24	6	AX052659	Sequence
C	45	13.6	56.7	24	6	AX445211	Sequence

ALIGNMENTS

RESULT 1
CS101223 LOCUS CS101223 24 bp DNA linear PAT 10-JUN-2005
DEFINITION Sequence 3 from Patent WO2005047540.
ACCESSION CS101223
VERSION CS101223.1 GI:67509720

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Pasha, A.O. and Ahsan, A.
TITLE Method of detecting predisposition to high altitude pulmonary edema
JOURNAL Patent: WO 2005047540-A 3 26-MAY-2005;
Council of Scientific and Industrial Research (IN)

FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGACG 24
|||||

Db 1 GATGCACAGCTGGGGAACAAGACG 24
|||||

RESULT 2

CQ979281 LOCUS CQ979281 26 bp DNA linear PAT 19-JAN-2005
DEFINITION Sequence 35 from Patent WO2005000888.
ACCESSION CQ979281
VERSION CQ979281.1 GI:57976534

KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct


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Best Local Similarity 93.8%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGAACAG 21
Db 16 ACAGCTGGGAACAG 1

RESULT 7
LOCUS AX588101 30 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 7 from Patent EP1253205.
ACCESSION AX588101
VERSION AX588101.1 GI:27899755
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Hofer,M., Kranz,H. and Klink,M.
AUTHORS Method of blocking amplification of selected sequences
TITLE Patent: EP 1253205-A 7 30-OCT-2002;
JOURNAL LION Bioscience AG (DE)
FEATURES
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1. .30
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGAACAGC 24
Db 6 GATGCACGAGGGGAGGAGAGG 29

RESULT 8
LOCUS AX642888 30 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7 from Patent WO2086155.
ACCESSION AX642888
VERSION AX642888.1 GI:28475108
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Hofer,M., Klink,M. and Kranz,H.
AUTHORS Method for the preferential nucleic acid synthesis reaction of one
TITLE or more selected regions of one or more target nucleic acids
JOURNAL Patent: WO 02086155-A 7 31-OCT-2002;
LION Bioscience AG (DE)
FEATURES
source
1. .30
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGAACAGC 24
Db 6 GATGCACGAGGGGAGGAGAGG 29

Best Local Similarity 93.8%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGAACAG 21
Db 16 ACAGCTGGGAACAG 1

RESULT 9
LOCUS CQ878645 21 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 17 from Patent EP1462521.
ACCESSION CQ878645
VERSION CQ878645.1 GI:53791103
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Deppert,W.W. and Dornreiter,I.
AUTHORS Human p53 splice variant displaying differential transcriptional
TITLE activity
JOURNAL Patent: EP 1462521-A 17 29-SEP-2004;
Deppert, Wolfgang Willi (DE)
FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer E1R"

ORIGIN
Query Match 59.2%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAACAAGA 22
Db 1 GCTCAGTGGGGACAAGA 19

RESULT 10
LOCUS CQ890107 21 bp DNA linear PAT 19-OCT-2004
DEFINITION Sequence 17 from Patent WO2004085468.
ACCESSION CQ890107
VERSION CQ890107.1 GI:54305801
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Deppert,W.W. and Dornreiter,I.
AUTHORS Novel human p53 splice variant displaying differential
TITLE transcriptional activity
JOURNAL Patent: WO 2004085468-A 17 07-OCT-2004;
Deppert, Wolfgang Willi (DE)
FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer E1R"

ORIGIN
Query Match 59.2%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAACAAGA 22
Db 1 GCTCAGTGGGGACAAGA 19

RESULT 11
LOCUS AX487198 22 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4498 from Patent WO2053728.
ACCESSION AX487198
VERSION AX487198.1 GI:22321346
KEYWORDS
```

```

SOURCE      Candida albicans
ORGANISM    Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
AUTHORS     Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE       Gene disruption methodologies for drug target discovery
JOURNAL     Patent: WO 02053728-A 4498 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES    Location/Qualifiers
            1..22
            /organism="Candida albicans"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5476"
ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GATGCACAGCTGGGGAACA 19
      ||||| ||||| |||||
Db      4 GATGGAGAGCTGGTGAACA 22

RESULT 12
E26387/c
LOCUS      E26387
DEFINITION Neutralized protein, polynucleotide encoding said protein and
            antibody recognizing said protein.
ACCESSION  E26387.1 GI:13025083
VERSION    JP 1999137257-A/14.
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 23)
AUTHORS    Motomi,N., Hideo,N., Mitsuhiro,Y. and Hideyuki,S.
TITLE      Neutralized protein, polynucleotide encoding said protein and
            antibody recognizing said protein
JOURNAL    Patent: JP 1999137257-A 14 25-MAY-1999;
            SUMITOMO ELECTRIC IND LTD
COMMENT    OS Unidentified
            PN JP 1999137257-A/14
            PD 25-MAY-1999
            PF 14-NOV-1997 JP 1997313211
            PR MOTOMI NAKADA,HIDEO NAKAMURA,MITSUHIRO YOSHIDA,HIDEYUKI SAYA
            PC C12N15/09,C07K14/47,C07K16/18,C12P21/02,C12Q1/68,G01N33/53//
            PC (C12N15/09,C12R1:91), (C12P21/02,C12R1:19),C12N15/00, PC
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source 1..23
            FT /organism="Unidentified".
            FT Location/Qualifiers
            1..23
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 23;
Best Local Similarity 84.2%; Pred. No. 9.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CACAGCTGGGGAACAAGAC 23
      ||||| ||||| |||||
Db      19 CCCAGCTGAGGACACAGCC 1

SOURCE      Candida albicans
ORGANISM    Candida albicans
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1
AUTHORS     Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE       Gene disruption methodologies for drug target discovery
JOURNAL     Patent: WO 02053728-A 4498 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES    Location/Qualifiers
            1..22
            /organism="Candida albicans"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5476"
ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GATGCACAGCTGGGGAACA 19
      ||||| ||||| |||||
Db      4 GATGGAGAGCTGGTGAACA 22

RESULT 13
A86551
LOCUS      A86551
DEFINITION Sequence 13 from Patent WO9839450.
ACCESSION  A86551
VERSION    A86551.1 GI:6735149
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified sequences.
            1 (bases 1 to 37)
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 37;
Best Local Similarity 77.3%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GATGCACAGCTGGGGAACAAGA 22
      ||||| ||||| |||||
Db      12 GATCCACAGGCTGGNAACAAGA 33

RESULT 14
BD082235
LOCUS      BD082235
DEFINITION Surface protein (SPsA protein) of streptococcus pneumoniae, deleted
            derivatives, expression system for said proteins and vaccine system
            with said proteins.
ACCESSION  BD082235.1 GI:22627845
VERSION    JP 2001524073-A/12.
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
            1 (bases 1 to 37)
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
REFERENCE   1 (bases 1 to 37)
AUTHORS    Chhatwal,G.S. and Hammerschmidt,S.
TITLE      Surface protein (SPsA protein) of streptococcus pneumoniae, deleted
            derivatives, expression system for said proteins and vaccine system
            with said proteins
JOURNAL    Patent: JP 2001524073-A 12 27-NOV-2001;
            GESELLSCHAFT FUR BIOTECHNOLOGISCHE FORSCHUNG MBH
COMMENT    PN JP 2001524073-A/12
            PD 27-NOV-2001
            PF 02-MAR-1998 JP 1998538137
            PR 03-MAR-1997 DE 19708537.7
            PI GURSHARAN SINGH CHHATWAL,SVEN HAMMERSCHMIDT
            PC C12N15/31,C07K14/315,A61K39/09,C12N15/70
            CC Strandedness: Single;
            CC Topology: Linear;
            CC /description = 'Primer'
            FH Key Location/Qualifiers
            FH Location/Qualifiers
            1..37
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 37;
Best Local Similarity 77.3%; Pred. No. 1.2e+05;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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VERSION AR167144.1 GI:16244
KEYWORDS


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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
1 (bases 1 to 20)
AUTHORS      Bos, J.L. and Van der Eb, A.J.
TITLE        Probes and methods for detecting activated ras oncogenes
JOURNAL      Patent: US 4871838-A 3 03-OCT-1989;
              The Board of Rijks Universiteit Leiden; Leiden;
FEATURES     NL;
              Location/Qualifiers
              source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 ACAGCTGGGGAACAAGA 22
        ||||| ||||| |||||
Db      20 ACAGCTGGGGAAGAAGA 4

RESULT 20
LOCUS    BD088354                20 bp DNA linear PAT 27-AUG-2002
DEFINITION
A method of arraying genome clone.
ACCESSION BD088354
VERSION    BD088354.1 GI:226333964
KEYWORDS   JP 2001321190-A/598.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
Soeda,E.
REFERENCE 1 (bases 1 to 20)
AUTHORS    Patent: JP 2001321190-A 598 20-NOV-2001;
              THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
JOURNAL    GENOTECHS
COMMENT    OS Artificial Sequence
PN JP 2001321190-A/598
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI ERICHI SORDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source 1..20
FT Location/Qualifiers
FEATURES     Location/Qualifiers
              source
              1..20
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGTGAAGAAGACG 20

RESULT 21
LOCUS    102471                20 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION
Sequence 3 from Patent US 4871838.
ACCESSION 102471
VERSION    102471.1 GI:270472
KEYWORDS

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
1 (bases 1 to 20)
AUTHORS      Bos, J.L. and Van der Eb, A.J.
TITLE        Probes and methods for detecting activated ras oncogenes
JOURNAL      Patent: US 4871838-A 3 03-OCT-1989;
              The Board of Rijks Universiteit Leiden; Leiden;
FEATURES     NL;
              Location/Qualifiers
              source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 11; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGTGAAGAAGACG 20

RESULT 23
LOCUS    CQ628621                20 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION
Sequence 3 from Patent US 4871838.
ACCESSION 102471
VERSION    102471.1 GI:270472
KEYWORDS

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LOCUS CQ628621 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13361 from Patent WO0192524.
ACCESSION CQ628621
VERSION CQ628621.1 GI:41678839
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
AUTHORS Myosin-like gene expressed in human heart and muscle
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13361 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES 1 Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 AGCTGGGGAACAGACG 24
Db 9 AGCTGGGGAACATGACG 25
RESULT 24
CQ628622
LOCUS CQ628622 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13362 from Patent WO0192524.
ACCESSION CQ628622
VERSION CQ628622.1 GI:41678840
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13362 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES 1 Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 AGCTGGGGAACAGACG 24
Db 8 AGCTGGGGAACATGACG 24
RESULT 25
CQ628623
LOCUS CQ628623 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13363 from Patent WO0192524.
ACCESSION CQ628623
VERSION CQ628623.1 GI:41678841
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
AUTHORS Myosin-like gene expressed in human heart and muscle
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13363 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES 1 Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 AGCTGGGGAACAGACG 24
Db 7 AGCTGGGGAACATGACG 23
RESULT 26
CQ628624
LOCUS CQ628624 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13364 from Patent WO0192524.
ACCESSION CQ628624
VERSION CQ628624.1 GI:41678842
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
AUTHORS Myosin-like gene expressed in human heart and muscle
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13364 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES 1 Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 AGCTGGGGAACAGACG 24
Db 6 AGCTGGGGAACATGACG 22
RESULT 27
CQ628625
LOCUS CQ628625 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13365 from Patent WO0192524.
ACCESSION CQ628625
VERSION CQ628625.1 GI:41678843
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13365 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES 1 Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13365 06-DEC-2001;
 Aeomica, Inc. (US)
FEATURES source
 1. .25
 /organism="Homo sapiens"
 /db_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
 ||||| ||||| |||||
Db 5 AGCTGGAGAACATGACG 21
 ||||| ||||| |||||

RESULT 28
LOCUS CQ628626 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13366 from Patent WO0192524.
ACCESSION CQ628626
VERSION CQ628626.1 GI:41678844
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13366 06-DEC-2001;
 Aeomica, Inc. (US)
FEATURES source
 1. .25
 /organism="Homo sapiens"
 /db_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
 ||||| ||||| |||||
Db 4 AGCTGGAGAACATGACG 20
 ||||| ||||| |||||

RESULT 29
LOCUS CQ628627 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13367 from Patent WO0192524.
ACCESSION CQ628627
VERSION CQ628627.1 GI:41678845
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13367 06-DEC-2001;

FEATURES source
 Aeomica, Inc. (US)
 Location/Qualifiers
 1. .25
 /organism="Homo sapiens"
 /db_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
 ||||| ||||| |||||
Db 3 AGCTGGAGAACATGACG 19
 ||||| ||||| |||||

RESULT 30
LOCUS CQ628628 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13368 from Patent WO0192524.
ACCESSION CQ628628
VERSION CQ628628.1 GI:41678846
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13368 06-DEC-2001;
 Aeomica, Inc. (US)
FEATURES source
 1. .25
 /organism="Homo sapiens"
 /db_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
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Db 2 AGCTGGAGAACATGACG 18
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RESULT 31
LOCUS CQ628629 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13369 from Patent WO0192524.
ACCESSION CQ628629
VERSION CQ628629.1 GI:41678847
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13369 06-DEC-2001;
 Aeomica, Inc. (US)
FEATURES source
 1. .25
 /organism="Homo sapiens"
 /db_type="unassigned DNA"

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ORIGIN
/db_xref="taxon:9606"

Query Match      57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 1 AGCTGGGGAACAATGACG 17
    ||||| ||||| |||||

RESULT 32
AR469684
LOCUS      25 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 13361 from patent US 6686188.
ACCESSION AR469684
VERSION AR469684.1 GI:42704741
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13361 03-FEB-2004;
Aersham PLC; Buckinghamshire;
GBX;
FEATURES
    source      Location/Qualifiers
    1..25
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 9 AGCTGGGGAACAATGACG 25
    ||||| ||||| |||||

RESULT 33
AR469685
LOCUS      25 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 13362 from patent US 6686188.
ACCESSION AR469685
VERSION AR469685.1 GI:42704742
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13362 03-FEB-2004;
Aersham PLC; Buckinghamshire;
GBX;
FEATURES
    source      Location/Qualifiers
    1..25
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 6 AGCTGGGGAACAATGACG 22
    ||||| ||||| |||||

RESULT 34
AR469686
LOCUS      25 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 13363 from patent US 6686188.
ACCESSION AR469686
VERSION AR469686.1 GI:42704743
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13363 03-FEB-2004;
Aersham PLC; Buckinghamshire;
GBX;
FEATURES
    source      Location/Qualifiers
    1..25
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 7 AGCTGGGGAACAATGACG 23
    ||||| ||||| |||||

RESULT 35
AR469687
LOCUS      25 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 13364 from patent US 6686188.
ACCESSION AR469687
VERSION AR469687.1 GI:42704744
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13364 03-FEB-2004;
Aersham PLC; Buckinghamshire;
GBX;
FEATURES
    source      Location/Qualifiers
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    /mol_type="genomic DNA"

ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 6 AGCTGGGGAACAATGACG 22
    ||||| ||||| |||||

RESULT 36
AR469688
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LOCUS AR469688 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13365 from patent US 6686188.
ACCESSION AR469688
VERSION AR469688.1 GI:42704745
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13365 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
||||| ||||| |||||
Db 5 AGCTGGAGAATGACG 21
||||| ||||| |||||
RESULT 37
LOCUS AR469689 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13366 from patent US 6686188.
ACCESSION AR469689
VERSION AR469689.1 GI:42704746
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13366 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
||||| ||||| |||||
Db 4 AGCTGGAGAATGACG 20
||||| ||||| |||||
RESULT 38
LOCUS AR469690 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13367 from patent US 6686188.
ACCESSION AR469690
VERSION AR469690.1 GI:42704747
KEYWORDS
SOURCE
ORGANISM

Unclassified.
1 (bases 1 to 25)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13367 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
||||| ||||| |||||
Db 3 AGCTGGAGAATGACG 19
||||| ||||| |||||
RESULT 39
LOCUS AR469691 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13368 from patent US 6686188.
ACCESSION AR469691
VERSION AR469691.1 GI:42704748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13368 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 AGCTGGGGAACAAGACG 24
||||| ||||| |||||
Db 2 AGCTGGAGAATGACG 18
||||| ||||| |||||
RESULT 40
LOCUS AR469692 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13369 from patent US 6686188.
ACCESSION AR469692
VERSION AR469692.1 GI:42704749
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13369 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;

Amersham PLC; Buckinghamshire;

GBX;

Location/Qualifiers

1. .25

/organism="unknown"

/mol_type="genomic DNA"

FEATURES

source

ORIGIN

Query Match 57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGACACAGACG 24

||||| ||||| |||||

Db 1 AGCTGGAGACATGACG 17

Search completed: December 13, 2005, 14:11:40
Job time : 1118.5 secs

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 947800
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-947800

Query Match 65.8%; Score 15.8; DB 9; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
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Db 1 GGACUGAUGGCAAGUACGA 19

RESULT 3

US-11-101-244-386342
; Sequence 386342, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 386342
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-386342

Query Match 60.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCAC 21
|||..|||:|||||
Db 1 GAGAGAUGGCAAGCAC 16

RESULT 4

US-11-083-784-386342
; Sequence 386342, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 386342
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-386342

Query Match 60.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCAC 21
|||..|||:|||||
Db 1 GAGAGAUGGCAAGCAC 16

RESULT 5

US-10-939-294A-17050
; Sequence 17050, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 17050
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17050

Query Match 59.2%; Score 14.2; DB 6; Length 32;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGC 19
|||..|||:|||||
Db 4 CAGCGGGGTGACGGGAAGC 22

RESULT 6

US-11-101-244-647873
; Sequence 647873, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-647873

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 9.7e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 CAGCGGAGTGATGGCAA 17
    ||||| :|| |||||
Db 2 CAGCGGACUGAAGGCAA 18

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```

RESULT 7
US-11-083-784-647873
; Sequence 647873, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-647873

```

```

Query Match      57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 9.7e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 CAGCGGAGTGATGGCAA 17
    ||||| :|| |||||
Db 2 CAGCGGACUGAAGGCAA 18

```

```

RESULT 8
US-11-101-244-882569/c
; Sequence 882569, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 882569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-882569

```

```

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 AGTCATGGCAAGCAC 21
    ||| ||||| |||||
Db 19 AGTAATGGCAAGCAC 5

```

```

RESULT 9
US-11-083-784-882569/c
; Sequence 882569, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 882569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-882569

```

```

Query Match      55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 7 AGTCATGGCAAGCAC 21
    ||| ||||| |||||
Db 19 AGTAATGGCAAGCAC 5

```

```

RESULT 10
US-11-101-244-248753
; Sequence 248753, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 248753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-248753

```

```

Query Match      55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 GCGGAGTGATGGCAAGCA 20
    |||||:|:|:|:|:|
Db 1 GCGGAGAGUGUCAUGCA 18

```

```

RESULT 11
US-11-101-244-287598
; Sequence 287598, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 287598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-287598

```

```

Query Match      55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 GCGGAGTGATGGCAAGCA 20
    |||||:|:|:|:|:|
Db 1 GCAAAGUGAUGGCAAGAA 18

```

```

RESULT 12
US-11-101-244-341923
; Sequence 341923, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 341923
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-341923

```

```

Query Match      55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 GCGGAGTGATGGCAAGCA 20
    |||||:|:|:|:|:|
Db 1 GCAGAGUGAUGUCAAGUA 18

```

```

RESULT 13
US-11-101-244-426653
; Sequence 426653, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 426653
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-426653

```

```

Query Match      55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 CAGCGGAGTGATGGCAAG 18
    |||||:|:|:|:|:|
Db 1 CAGCUGAGAUUGGCAAG 18

```

```

RESULT 14
US-11-101-244-770754
; Sequence 770754, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 770754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-770754
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 GAGTGTGGCAAGCAGCA 23
|||:|||||:|||||
Db 2 GAGUGACGCAAGAAGCA 19
```

```
RESULT 15
US-11-083-784-248753
; Sequence 248753, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 248753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-248753
```

```
Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 GCGGAGTGTGGCAAGCA 20
|||||:|||||:|||||
Db 1 GCGGAGAGAGUUGCAUGCA 18
```

```
RESULT 16
US-11-083-784-287598
; Sequence 287598, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 287598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-287598
```

```
Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 GCGGAGTGTGGCAAGCA 20
|||:|||||:|||||
Db 1 GCAAAGUGAUGCAAGAA 18
```

```
RESULT 17
US-11-083-784-341923
; Sequence 341923, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 341923
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-341923
```

```
Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 GCGGAGTGTGGCAAGCA 20
|||:|||||:|||||
Db 1 GCAGAGUGAUGCAAGAA 18
```

```
RESULT 18
US-11-083-784-426653
; Sequence 426653, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 426653
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-426653

Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAG 18
||| ||| ||| ||| |||
Db 1 CAGCUGAGAUUGGCAAG 18

RESULT 19
US-11-083-784-770754
; Sequence 770754, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 770754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-770754

Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 GAGTGATGGCAAGCAGCA 23
||| ||| ||| ||| |||
Db 2 GAGUGACGCGCAAGAGGA 19

RESULT 20
US-10-939-294A-17174
; Sequence 17174, Application US/10939294A

; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17174
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17174

Query Match 55.0%; Score 13.2; DB 6; Length 32;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAG 18
||| ||| ||| ||| |||
Db 8 CAGCGGGTGACGGCGAG 25

RESULT 21
US-11-101-244-332886
; Sequence 332886, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 332886
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-332886

Query Match 54.2%; Score 13; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAGTGATGGCAAG 18
||| ||| ||| |||
Db 4 GAGUGAGGCGCAAG 16

RESULT 22
US-11-083-784-332886
; Sequence 332886, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 332886
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-332886

Query Match 54.2%; Score 13; DB 9; Length 19;
Best Local Similarity 84.6%; Pred. No. 2.2e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAG 18
|||:|||||
Db 4 GAGUGAUGGCAAG 16

RESULT 23

US-10-770-726-27035
; Sequence 27035, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27035
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27035

Query Match 54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAG 18
|||:|||||
Db 3 GAGTGTGGCAAG 15

RESULT 24

US-10-770-726-27036
; Sequence 27036, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)

Query Match 54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27036
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-27036

Query Match 54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAG 18
|||:|||||
Db 1 GAGUGAUGGCAAG 13

RESULT 25

US-10-770-726-27533
; Sequence 27533, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27533
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27533

Query Match 54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAG 18
|||:|||||
Db 7 GAGTGTGGCAAG 19

RESULT 26

US-10-770-726-27534
; Sequence 27534, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27534
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-27534

Query Match 54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY      6 GAGTGATGGCAAG 18
DB      5 GAGUGAUGGCAAG 17

RESULT 27
US-10-770-726-27536
; Sequence 27536, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27536
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27536

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
DB      1 GAGTGATGGCAAG 13

RESULT 30
US-10-770-726-27989
; Sequence 27989, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27989
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27989

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
DB      3 GAGTGATGGCAAG 15

RESULT 31
US-10-770-726-27990
; Sequence 27990, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27990
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-770-726-27990

QY      6 GAGTGATGGCAAG 18
DB      5 GAGUGAUGGCAAG 17

RESULT 28
US-10-770-726-27537
; Sequence 27537, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27537
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1
US-10-770-726-27537

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
DB      4 GAGTGATGGCAAG 16

RESULT 29
US-10-770-726-27539
; Sequence 27539, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
```

```
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28073
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-28073

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAGTGATGGCAAG 18
Db      1 GAGUGAUGGCAAG 13

RESULT 32
US-10-770-726-28073
; Sequence 28073, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28073
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-28073

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAGTGATGGCAAG 18
Db      7 GAGTGATGGCAAG 19

RESULT 33
US-10-770-726-28074
; Sequence 28074, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28074
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
; US-10-770-726-28074

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAGTGATGGCAAG 18
Db      5 GAGUGAUGGCAAG 17

RESULT 34
US-10-770-726-28076
; Sequence 28076, Application US/10770726
```

```
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28076
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-28076

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAGTGATGGCAAG 18
Db      4 GAGTGATGGCAAG 16

RESULT 35
US-10-770-726-28077
; Sequence 28077, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28077
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
; US-10-770-726-28077

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAGTGATGGCAAG 18
Db      2 GAGUGAUGGCAAG 14

RESULT 36
US-10-770-726-28079
; Sequence 28079, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28079
```



```
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-28079

Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGCGCAAG 18
Db      1 GAGTGATGCGCAAG 13

RESULT 37
US-10-939-294A-17960
; Sequence 17960, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CFR D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17960
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17960

Query Match          54.2%; Score 13; DB 6; Length 32;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CAGCGGAGTGATGGCAAGCAC 21
Db      4 CAGCGGGGTGACGCGCAACGC 24

RESULT 38
US-11-101-244-385942
; Sequence 385942, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385942
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-385942

Query Match          53.3%; Score 12.8; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 GGAGTGATGGCAAGCA 20
Db      1 GGAGUGAUGGCAGGUA 16

RESULT 39
US-11-101-244-394642
; Sequence 394642, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 394642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-394642

Query Match          53.3%; Score 12.8; DB 8; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 GGAGTGATGGCAAGCA 20
Db      2 GGAGUGACUGCAAGCA 17

RESULT 40
US-11-101-244-394667
; Sequence 394667, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 394667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-394667
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Query Match 53.1%; Score 12.8; DB 8; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCA 20
||||:||||
Db 1 GGAGUGACUGCAAGCA 16
||||:||||

Search completed: December 13, 2005, 16:24:34
Job time : 214.5 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:21:57 ; Search time 660 Seconds
(without alignments)
300.705 Million cell updates/sec

Title: US-10-713-137-2
Perfect score: 24
Sequence: 1 cagcggagtgcgaagcagcagc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	100.0	24	9	US-10-713-137-2
2	18.2	75.8	37	3	US-09-780-533A-4303
3	17.2	71.7	37	3	US-09-730-289B-2709
4	17.2	71.7	37	3	US-09-776-474-1941
5	16.8	70.0	36	7	US-10-712-672-4389
6	16.6	69.2	25	10	US-11-060-756-223011
7	16.6	69.2	37	3	US-09-730-289B-2718
8	16.6	69.2	37	3	US-09-780-533A-4266
9	16.6	69.2	37	3	US-09-927-046-3502
10	16.6	69.2	37	3	US-09-877-478-4013
11	16.6	69.2	37	3	US-09-930-423-2746
12	16.6	69.2	37	3	US-09-930-423-2764
13	16.6	69.2	37	3	US-09-930-423-2765
14	16.6	69.2	37	3	US-09-930-423-2786
15	16.6	69.2	37	3	US-09-745-237A-2746
16	16.6	69.2	37	3	US-09-745-237A-2764
17	16.6	69.2	37	3	US-09-745-237A-2765
18	16.6	69.2	37	3	US-09-745-237A-2786
19	16.6	69.2	37	3	US-10-342-902-4013
20	16.6	69.2	37	7	US-10-669-841-8904
21	16.2	67.5	37	3	US-09-780-533A-4274
22	16.2	67.5	37	3	US-09-877-478-3997
23	16.2	67.5	37	7	US-10-342-902-3997

24	16.2	67.5	37	7	US-10-669-841-8888	Sequence 8888, Ap
c 25	16	66.7	18	9	US-10-182-049-35	Sequence 35, Appl
c 26	16	66.7	25	7	US-10-719-956-607979	Sequence 607979,
27	15.8	65.8	25	10	US-11-036-317-435997	Sequence 435997,
28	15.8	65.8	36	7	US-10-138-674-15256	Sequence 15256, A
29	15.8	65.8	36	7	US-10-138-674-15277	Sequence 15277, A
30	15.8	65.8	36	7	US-10-387-949A-15256	Sequence 15256, A
31	15.8	65.8	36	7	US-10-287-949A-15277	Sequence 15277, A
32	15.8	65.8	36	7	US-10-712-672-4241	Sequence 4241, Ap
33	15.8	65.8	36	7	US-10-712-672-4246	Sequence 4246, Ap
34	15.8	65.8	36	7	US-10-712-672-4375	Sequence 4375, Ap
35	15.8	65.8	36	7	US-10-712-672-4498	Sequence 4498, Ap
36	15.8	65.8	37	3	US-09-780-533A-4335	Sequence 4335, Ap
37	15.8	65.8	37	3	US-09-927-046-3492	Sequence 3492, Ap
38	15.8	65.8	37	3	US-09-927-046-3526	Sequence 3526, Ap
39	15.8	65.8	37	3	US-09-927-046-3549	Sequence 3549, Ap
40	15.8	65.8	37	3	US-09-776-474-1927	Sequence 1927, Ap
41	15.8	65.8	37	3	US-09-780-164-1810	Sequence 1810, Ap
42	15.6	65.0	25	10	US-11-060-756-248181	Sequence 248181,
43	15.6	65.0	37	3	US-09-780-533A-4293	Sequence 4293, Ap
44	15.6	65.0	37	3	US-09-780-533A-4302	Sequence 4302, Ap
45	15.6	65.0	37	3	US-09-780-533A-4309	Sequence 4309, Ap

ALIGNMENTS

RESULT 1
US-10-713-137-2
; Sequence 2, Application US/10713137
; Publication No. US20050106573A1
; GENERAL INFORMATION:
; APPLICANT: Pasha, Abdul Qadar Mohammad
; APPLICANT: Ahsan, Aarif
; TITLE OF INVENTION: A method of detection of predisposition
; FILE REFERENCE: 09755-0018US1
; CURRENT APPLICATION NUMBER: US/10/713,137
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-713-137-2

Query Match 100.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCGGAGTGATGGCAGCAGCAGC 24
| | | | | | | | | | | | | | | | | |
Db 1 CAGCGGAGTGATGGCAGCAGCAGC 24

RESULT 2
US-09-780-533A-4303
; Sequence 4303, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797

; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4303
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4303

Query Match 75.8%; Score 18.2; DB 3; Length 37;
Best Local Similarity 78.3%; Pred. No. 90;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACGGAGTGATGCGCAAGCACGA 23
||| ||||:|||||
Db 1 CAGAGGAGUGAUGGCAUGCACUA 23

RESULT 3
US-09-730-289B-2709
; Sequence 2709, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2709
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-730-289B-2709

Query Match 71.7%; Score 17.2; DB 3; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.7e+02;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACGGAGTGATGCGCAAGCACGA 23
||| ||||:|||||
Db 2 AGCUGAGUGAUGGCAUGCACUA 23

RESULT 4
US-09-776-474-1941
; Sequence 1941, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boehr, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1941
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1941

Query Match 71.7%; Score 17.2; DB 3; Length 37;
Best Local Similarity 77.3%; Pred. No. 2.7e+02;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACGGAGTGATGCGCAAGCACGA 23
||| ||||:|||||
Db 2 AGAGGAGUGAUGGCAUGCACUA 23

RESULT 5
US-10-712-672-4389
; Sequence 4389, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4389
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4389

Query Match 70.0%; Score 16.8; DB 7; Length 36;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGAGTGATGCGCAAGCACGA 23
||| ||||:|||||
Db 1 CGGAGUGAUGGCAUGCACUA 20

RESULT 6
US-11-060-756-223011
; Sequence 223011, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 223011
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe

US-11-060-756-223011

Query Match 69.2%; Score 16.6; DB 10; Length 25;
Best Local Similarity 82.6%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGATGGCAAGCAGC 24
Db 2 AGCGGAGTGACAGTAAGCAGGAC 24

RESULT 7

US-09-730-289B-2718
; Sequence 2718, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MEH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2718
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-730-289B-2718

Query Match 69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23
Db 1 CAGAGAAGUGAUGGCAUGCAGCA 23

RESULT 8

US-09-780-533A-4266
; Sequence 4266, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4266
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4266

Query Match 69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23
Db 1 CAGGGGCGUGAUGGCAUGCAGCA 23

RESULT 9

US-09-927-046-3502
; Sequence 3502, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3502
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3502

Query Match 69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23
Db 1 CAGGGUAGUGAUGGCAUGCAGCA 23

RESULT 10

US-09-877-478-4013
; Sequence 4013, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MEH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4013
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-4013

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:|:|:|:|:|:|
DB 1 CAGCCUAGUGAUGGCAUGCACUA 23

RESULT 11
US-09-930-423-2746
; Sequence 2746, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2746
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2746

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:|:|:|:|:|:|
DB 1 CAGCCUAGUGAUGGCAUGCACUA 23

RESULT 12
US-09-930-423-2764
; Sequence 2764, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2764
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2764

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CGCGCGGUGAUGGCAUGCACUA 23

RESULT 13
US-09-930-423-2765
; Sequence 2765, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2765
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2765

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CGCGAGUGAUGGCAUGCACUA 23

RESULT 14
US-09-930-423-2786
; Sequence 2786, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2786
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2786

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CGCGAGUGAUGGCAUGCACUA 23

RESULT 15
US-09-745-237A-2746
; Sequence 2746, Application US/09745237A
; Publication No. US20030143708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2746
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2746

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGGGGUGAUGGCAUGCACUA 23

RESULT 16
US-09-745-237A-2764
; Sequence 2764, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2764
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2764

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGGGGUGAUGGCAUGCACUA 23

RESULT 17
US-09-745-237A-2765
; Sequence 2765, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2765
```

```
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2765

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGAGAGUGAUGGCAUGCACUA 23

RESULT 18
US-09-745-237A-2786
; Sequence 2786, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2786
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2786

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CAGCGGGGUGAUGGCAUGCACUA 23

RESULT 19
US-10-342-902-4013
; Sequence 4013, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
```


;; PRIOR APPLICATION NUMBER: US 09/436,430
;; PRIOR FILING DATE: 1999-11-08
;; NUMBER OF SEQ ID NOS: 6592
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 4013
;; LENGTH: 37
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-4013

Query Match 69.2%; Score 16.6; DB 7; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCACGA 23
||| |||:|||||
Db 1 CAGCCUAGUGAUGGCAUGACUA 23

RESULT 20
US-10-669-841-8904
;; Sequence 8904, Application US/10669841
;; Publication No. US20040127446A1
;; GENERAL INFORMATION:
;; APPLICANT: Sirna Therapeutics, Inc.
;; APPLICANT: Lawrence, Blatt
;; APPLICANT: Dennis, Macejak
;; APPLICANT: James, McSwiggen
;; APPLICANT: David, Morrissey
;; APPLICANT: Pamela, Pavco
;; APPLICANT: Patricia, Lee
;; APPLICANT: Kenneth, Draper
;; APPLICANT: Elisabeth, Roberts
;; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
;; TITLE OF INVENTION: VIRUS REPLICATION
;; FILE REFERENCE: 400/04205 (MBH02-249-E)
;; CURRENT APPLICATION NUMBER: US/10/669,841
;; CURRENT FILING DATE: 2003-09-23
;; PRIOR APPLICATION NUMBER: PCT/US02/09187
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: US 60/296,876
;; PRIOR FILING DATE: 2001-06-08
;; PRIOR APPLICATION NUMBER: US 60/335,059
;; PRIOR FILING DATE: 2001-10-24
;; PRIOR APPLICATION NUMBER: US 60/337,055
;; PRIOR FILING DATE: 2001-12-05
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 60/363,124
;; PRIOR FILING DATE: 2002-03-11
;; PRIOR APPLICATION NUMBER: US 09/817,879
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: US 09/740,332
;; PRIOR FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: US 09/611,931
;; PRIOR FILING DATE: 2000-07-07
;; PRIOR APPLICATION NUMBER: US 09/504,321
;; PRIOR FILING DATE: 2000-02-15
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 16207
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 8904
;; LENGTH: 37
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-669-841-8904

Query Match 69.2%; Score 16.6; DB 7; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGCGAGTGATGGCAAGCACGA 23
||| |||:|||||
Db 1 CAGCCUAGUGAUGGCAUGACUA 23
RESULT 21
US-09-780-533A-4274
;; Sequence 4274, Application US/09780533A
;; Publication No. US20030060611A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.
;; APPLICANT: Blatt, Larry
;; APPLICANT: McSwiggen, Jim
;; APPLICANT: Chowrira, Bharat
;; APPLICANT: Haerberli, Pete
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;; FILE REFERENCE: MBH00,878-A (400/011)
;; CURRENT APPLICATION NUMBER: US/09/780,533A
;; CURRENT FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: US 60/181,797
;; PRIOR FILING DATE: 2000-02-11
;; NUMBER OF SEQ ID NOS: 6679
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4274
;; LENGTH: 37
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4274

Query Match 67.5%; Score 16.2; DB 3; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGGCAAGCACGA 23
||| |||:|||||
Db 3 GGGGAGUGAUGGCAUGACUA 23

RESULT 22
US-09-877-478-3997
;; Sequence 3997, Application US/09877478
;; Publication No. US20030068301A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.
;; APPLICANT: Draper, Kenneth
;; APPLICANT: Blatt, Larry
;; APPLICANT: McSwiggen, Jim
;; APPLICANT: Morrissey, Dave
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
;; FILE REFERENCE: MBH00-845-H (400/029)
;; CURRENT APPLICATION NUMBER: US/09/877,478
;; CURRENT FILING DATE: 2001-12-31
;; PRIOR APPLICATION NUMBER: US 07/882,712
;; PRIOR FILING DATE: 1992-05-14
;; PRIOR APPLICATION NUMBER: US 09/531,025
;; PRIOR FILING DATE: 2000-03-20
;; PRIOR APPLICATION NUMBER: US 09/636,385
;; PRIOR FILING DATE: 2000-08-09
;; PRIOR APPLICATION NUMBER: US 09/696,347
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 08/193,627
;; PRIOR FILING DATE: 1994-02-07
;; PRIOR APPLICATION NUMBER: US 08/433,993
;; PRIOR FILING DATE: 1995-05-04
;; PRIOR APPLICATION NUMBER: US 08/434,504
;; PRIOR FILING DATE: 1995-05-04
;; PRIOR APPLICATION NUMBER: US 09/436,430
;; PRIOR FILING DATE: 1999-11-08
;; NUMBER OF SEQ ID NOS: 6586

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3997
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-3997

Query Match          67.5%; Score 16.2; DB 3; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAAGCACGA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 23
US-10-342-902-3997
; Sequence 3997, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Draper, Kenneth
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3997
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-3997

Query Match          67.5%; Score 16.2; DB 7; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAAGCACGA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 24
US-10-669-841-8888
; Sequence 8888, Application US/10669841
; Publication No. US2004012746A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
```

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; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8888
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-669-841-8888

Query Match          67.5%; Score 16.2; DB 7; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAAGCACGA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 25
US-10-182-049-35/c
; Sequence 35, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRES
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-182-049-35

Query Match 66.7%; Score 16; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGATGGCAAGCAGC 24
|||||
DB 18 TGATGGCAAGCAGC 3

RESULT 26

US-10-719-956-607979/c

; Sequence 607979, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 607979

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-607979

Query Match 66.7%; Score 16; DB 7; Length 25;
Best Local Similarity 79.2%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGC 24
|||||
DB 25 CAGCAGAGTGTGGCAGTCACGTC 2

RESULT 27

US-11-036-317-435997

; Sequence 435997, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 435997

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-435997

Query Match 65.8%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCAGC 24
|||
DB 1 GACTGATGGCAAGCATGAC 19

RESULT 28

US-10-138-674-15256

; Sequence 15256, Application US/10138674

; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15256

; LENGTH: 36

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-15256

Query Match 65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23
|||||
DB 2 GGAGUGAUGGCAUGCACUA 20

RESULT 29

US-10-138-674-15277

; Sequence 15277, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15277

; LENGTH: 36

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-15277

Query Match 65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23
|||||
DB 2 GGAGUGAUGGCAUGCACUA 20

RESULT 30

US-10-287-949A-15256

; Sequence 15256, Application US/10287949A

; Publication No. US20040102189A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MH000-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15256
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-15256

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 31
US-10-287-949A-15277
; Sequence 15277, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MH000-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15277
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-15277

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 32
US-10-712-672-4241
; Sequence 4241, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MH000-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
```

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; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4241
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4241

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 33
US-10-712-672-4246
; Sequence 4246, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MH000-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4246
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4246

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 34
US-10-712-672-4375
; Sequence 4375, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
```

; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4375
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4375

Query Match 65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 35
US-10-712-672-4498
; Sequence 4498, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4498
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4498

Query Match 65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 36
US-09-780-533A-4335
; Sequence 4335, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry

; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4335
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-4335

Query Match 65.8%; Score 15.8; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
||||:|||||
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 37
US-09-927-046-3492
; Sequence 3492, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3492
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3492

Query Match 65.8%; Score 15.8; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
||||:|||||
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 38
US-09-927-046-3526
; Sequence 3526, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim

```
; APPLICANT: Avers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3526
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3526

Query Match      65.8%; Score 15.8; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 39
US-09-927-046-3549
; Sequence 3549, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Avers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3549
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-3549

Query Match      65.8%; Score 15.8; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 40
US-09-776-474-1927
; Sequence 1927, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
```

```
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CI)
; FILE REFERENCE: MSHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1927
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1927

Query Match      65.8%; Score 15.8; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 5 GGAGUGAUGGCAUGCACUA 23

Search completed: December 13, 2005, 16:17:14
Job time : 661 secs
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:14:34 ; Search time 104.5 Seconds
(without alignments)
408.244 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcggagtgcgaagcagac 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/pp COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	65.8	36	3	US-09-371-772B-12979 Sequence 12979, A
2	15.8	65.8	36	3	US-09-371-772B-13000 Sequence 13000, A
3	15.8	65.8	36	3	US-09-479-005A-597 Sequence 597, App
4	15.2	63.3	36	3	US-09-371-772B-12711 Sequence 12711, A
5	15.2	63.3	36	3	US-09-371-772B-12725 Sequence 12725, A
6	15.2	63.3	36	3	US-09-371-772B-14177 Sequence 14177, A
7	15.2	63.3	36	3	US-09-371-772B-14200 Sequence 14200, A
8	15.2	63.3	36	3	US-09-479-005A-825 Sequence 825, App
9	15.2	63.3	36	3	US-09-479-005A-1014 Sequence 1014, App
10	15	62.5	39	3	US-09-430-221-27 Sequence 27, Appl
11	14.8	61.7	25	3	US-09-866-108A-4012 Sequence 4012, App
12	14.8	61.7	25	3	US-09-866-108A-4013 Sequence 4013, App
13	14.8	61.7	25	3	US-09-866-108A-4014 Sequence 4014, App
14	14.8	61.7	25	3	US-09-866-108A-4015 Sequence 4015, App
15	14.8	61.7	25	3	US-09-866-108A-4016 Sequence 4016, App
16	14.8	61.7	25	3	US-09-866-108A-4017 Sequence 4017, App
17	14.8	61.7	25	3	US-09-866-108A-4018 Sequence 4018, App
18	14.8	61.7	25	3	US-09-866-108A-4019 Sequence 4019, App
19	14.8	61.7	36	3	US-09-371-772B-12719 Sequence 12719, A
20	14.8	61.7	36	3	US-09-371-772B-12797 Sequence 12797, A
21	14.8	61.7	36	3	US-09-371-772B-12964 Sequence 12964, A
22	14.8	61.7	36	3	US-09-371-772B-13173 Sequence 13173, A
23	14.8	61.7	36	3	US-09-371-772B-14087 Sequence 14087, A
24	14.8	61.7	36	3	US-09-371-772B-14110 Sequence 14110, A

25	14.8	61.7	36	3	US-09-371-772B-14162 Sequence 14162, A
26	14.8	61.7	36	3	US-09-479-005A-665 Sequence 665, App
27	14.8	61.7	36	3	US-09-479-005A-785 Sequence 785, App
28	14.8	61.7	36	3	US-09-479-005A-938 Sequence 938, App
29	14.4	60.0	25	3	US-09-396-196G-42756 Sequence 42756, A
30	14.4	60.0	35	9	5519127-6 Patent No. 5519127
31	14.2	59.2	36	3	US-09-371-772B-12724 Sequence 12724, A
32	14.2	59.2	36	3	US-09-371-772B-12727 Sequence 12727, A
33	14.2	59.2	36	3	US-09-371-772B-12754 Sequence 12754, A
34	14.2	59.2	36	3	US-09-371-772B-12767 Sequence 12767, A
35	14.2	59.2	36	3	US-09-371-772B-12819 Sequence 12819, A
36	14.2	59.2	36	3	US-09-371-772B-12861 Sequence 12861, A
37	14.2	59.2	36	3	US-09-371-772B-12890 Sequence 12890, A
38	14.2	59.2	36	3	US-09-371-772B-12839 Sequence 12839, A
39	14.2	59.2	36	3	US-09-371-772B-12962 Sequence 12962, A
40	14.2	59.2	36	3	US-09-371-772B-12978 Sequence 12978, A
41	14.2	59.2	36	3	US-09-371-772B-12980 Sequence 12980, A
42	14.2	59.2	36	3	US-09-371-772B-13014 Sequence 13014, A
43	14.2	59.2	36	3	US-09-371-772B-13062 Sequence 13062, A
44	14.2	59.2	36	3	US-09-371-772B-13065 Sequence 13065, A
45	14.2	59.2	36	3	US-09-371-772B-13067 Sequence 13067, A

ALIGNMENTS

RESULT 1

US-09-371-772B-12979 ; Sequence 12979, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12979
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12979

Query Match 65.8%; Score 15.8; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 4.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGCGAAGCAGCA 23
|||||:|||||
Db 2 GGAGUGAUGGCAUGCAGCA 20
|||||:|||||

RESULT 2

US-09-371-772B-13000 ; Sequence 13000, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan


```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13000
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-13000

Query Match      65.8%; Score 15.8; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 4.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTCATGCCAGCACGA 23
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 3
US-09-479-005A-597
; Sequence 597, Application US/09479005A
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 597
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-597

Query Match      65.8%; Score 15.8; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 4.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTCATGCCAGCACGA 23
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 4
US-09-371-772B-12711
; Sequence 12711, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12711
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12711

Query Match      63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGTCATGCCAAGCACGA 23
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 5
US-09-371-772B-12725
; Sequence 12725, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12725
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12725

Query Match      63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGTCATGCCAAGCACGA 23
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 6
US-09-371-772B-14177
; Sequence 14177, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14177
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14177

Query Match 63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23
| | | | | | | | | | | | | | | |
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 7
US-09-371-772B-14200
; Sequence 14200, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14200
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14200

Query Match 63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23
| | | | | | | | | | | | | | | |
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 8
US-09-479-005A-825
; Sequence 825, Application US/09479005A

; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 825
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-825

Query Match 63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23
| | | | | | | | | | | | | | | |
Db 1 CGUAGUGAUGGCAUGCACUA 20

RESULT 9
US-09-479-005A-1014
; Sequence 1014, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1014
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-1014

Query Match 63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23
| | | | | | | | | | | | | | | |
Db 1 CGGGGUGAUGGCAUGCACUA 20

RESULT 10
US-09-430-221-27/c
; Sequence 27, Application US/09430221
; Patent No. 6521425
; GENERAL INFORMATION:
; APPLICANT: Perler, Francine B.

; PRIOR APPLICATION NUMBER: PCT/US01/006669

Overall Match 61 78. Score 14

```
Best Local Similarity 88.9%; Pred. No. 1.2e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0;

QY 5 GGAGTGATGCGAAGCAGC 22
    ||||| |||||
Db 4 GGAGTGAAGGGAAGCAGC 21

RESULT 16
US-09-866-108A-4017
; Sequence 4017, Application US/09866108A
; Patent No. 6686188
; FILE REFERENCE: AEOMICA-7
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4017
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4017

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGCGAAGCAGC 22
    ||||| |||||
Db 3 GGAGTGAAGGGAAGCAGC 20

RESULT 17
US-09-866-108A-4018
; Sequence 4018, Application US/09866108A
; Patent No. 6686188
; FILE REFERENCE: AEOMICA-7
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4017
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4017

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGCGAAGCAGC 22
    ||||| |||||
Db 3 GGAGTGAAGGGAAGCAGC 20

RESULT 17
US-09-866-108A-4018
; Sequence 4018, Application US/09866108A
; Patent No. 6686188
; FILE REFERENCE: AEOMICA-7
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4018
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4018

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGCGAAGCAGC 22
    ||||| |||||
Db 2 GGAGTGAAGGGAAGCAGC 19

RESULT 18
US-09-866-108A-4019
; Sequence 4019, Application US/09866108A
; Patent No. 6686188
; FILE REFERENCE: AEOMICA-7
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4018
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4019
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6586188
; SEQ ID NO 4019
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-4019

Query Match      61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACG 22
Db 1 GGAGTGAAGGCAAGCACG 18

RESULT 19
US-09-371-772B-12719
; Sequence 12719, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12719
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12719

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 20
US-09-371-772B-12797
; Sequence 12797, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12797
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12797

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 21
US-09-371-772B-12964
; Sequence 12964, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12964
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12964

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 22
US-09-371-772B-13173
; Sequence 13173, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13173
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-13173

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23
|||:|||||
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 23
US-09-371-772B-14087
; Sequence 14087, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14087
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14087

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23
|||:|||||
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 24
US-09-371-772B-14110

; Sequence 14110, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14110
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14110

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23
|||:|||||
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 25
US-09-371-772B-14162
; Sequence 14162, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14162
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-14162

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23
|||:|||||
Db 3 GAGUGAUGGCAUGCACUA 20

```
RESULT 26
US-09-479-005A-665
; Sequence 665, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 665
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-665

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 27
US-09-479-005A-785
; Sequence 785, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 785
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-785

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 28
US-09-479-005A-938
; Sequence 938, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 938
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-938

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 29
US-09-396-196G-42756/c
; Sequence 42756, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 42756
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-42756

Query Match 60.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGTCGCAAGCACGAC 24
Db 24 CAGCAGGCTGTGTCGCAAGCACGAC 1

RESULT 30
5519127-6/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
```

```
; Sequence 938, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 938
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-938

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 29
US-09-396-196G-42756/c
; Sequence 42756, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 42756
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-42756

Query Match 60.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGTCGCAAGCACGAC 24
Db 24 CAGCAGGCTGTGTCGCAAGCACGAC 1

RESULT 30
5519127-6/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
```



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; APPLICATION NUMBER: US/07/826,657
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 392,679
; FILING DATE: 11-AUG-1989
; SEQ ID NO:6:
; LENGTH: 35
5519127-6

Query Match      60.0%; Score 14.4; DB 9; Length 35;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGC 24
    ||||| ||||| ||||| |||||
Db 25 CAGCGGGCTGTGGCAACGATGAC 2

RESULT 31
US-09-371-772B-12724
; Sequence 12724, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12724
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12724
```

```
Query Match      59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23
    ||||| ||||| ||||| |||||
Db 2 GCAGUGAUGGCAUGCACUA 20

RESULT 32
US-09-371-772B-12727
; Sequence 12727, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

```
; APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12727
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12727

Query Match      59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23
    ||||| ||||| ||||| |||||
Db 2 GAAGUGAUGGCAUGCACUA 20

RESULT 33
US-09-371-772B-12754
; Sequence 12754, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12754
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12754

Query Match      59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23
    ||||| ||||| ||||| |||||
Db 2 GGAUUGAUGGCAUGCACUA 20

RESULT 34
US-09-371-772B-12767
; Sequence 12767, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
```

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12767
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12767

Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
|||:|||||
Db 2 GUAGUGAUGGCAUGCACUA 20

RESULT 35

US-09-371-772B-12819
; Sequence 12819, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12819
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12819

Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
|||:|||||
Db 2 GGAUGAUGGCAUGCACUA 20

RESULT 36

US-09-371-772B-12861
; Sequence 12861, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12861
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12861

Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
|||:|||||
Db 2 GGUGUGAUGGCAUGCACUA 20

RESULT 37

US-09-371-772B-12890
; Sequence 12890, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12890
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12890

Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
|||:|||||
Db 2 GGUGUGAUGGCAUGCACUA 20

RESULT 38

US-09-371-772B-12939
; Sequence 12939, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12939
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12939
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```
Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 GGAGTGTGGCAAGCACGA 23
| | | | | | | | | |
Db 2 GAAGUGAUGGCAUGCACUA 20
```

RESULT 39

```
US-09-371-772B-12962
; Sequence 12962, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12962
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12962
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Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 5 GGAGTGTGGCAAGCACGA 23
| | | | | | | | | |
Db 2 GAAGUGAUGGCAUGCACUA 20
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RESULT 40

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US-09-371-772B-12978
; Sequence 12978, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12978
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12978
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Query Match 59.2%; Score 14.2; DB 3; Length 36;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 5 GGAGTGTGGCAAGCACGA 23
| | | | | | | | | |
Db 2 GCAGUGAUGGCAUGCACUA 20
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Search completed: December 13, 2005, 15:54:59
Job time : 105.5 secs
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Query Match      63.3%; Score 15.2; DB 9; Length 50;
Best Local Similarity 85.0%; Pred. No. 3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  CGGAGTCATGGCAAGCACGA 23
      |||||

```



```

15539471
PUBMED
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
1. .42
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_3_07_e21"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 55.8%; Score 13.4; DB 1; Length 42;
Best Local Similarity 73.9%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAGCA 23
DB 40 CACCGCGTCAAGTAAGCTCGA 18

RESULT 5
CF331176/c
LOCUS
DEFINITION NACL--07-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-D03, mRNA
sequence.
ACCESSION CF331176
VERSION CF331176.1 GI:33810575
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 40)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--07-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-ROPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 55.0%; Score 13.2; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAG 18
DB 25 CATCGGAGTGATGGGAGG 8

15539593
PUBMED
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
1. .42
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_3_07_e21"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 55.8%; Score 13.4; DB 1; Length 42;
Best Local Similarity 73.9%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAGCA 23
DB 40 CACCGCGTCAAGTAAGCTCGA 18

RESULT 6
AV839593
LOCUS
DEFINITION AV839593 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone rciad06f24, mRNA sequence.
ACCESSION AV839593.1 GI:16783744
VERSION AV839593
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 40)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sato@acidian.zool.kyoto-u.ac.jp.
FEATURES
source
1. .40
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rciad06f24"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

ORIGIN
Query Match 54.2%; Score 13; DB 1; Length 40;
Best Local Similarity 66.7%; Pred. No. 2.9e+05;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAGCAGC 24
DB 8 CNGCGGTTCGCGGCANGCANGAC 31

RESULT 7
AI019594/c
LOCUS
DEFINITION AI019594 ua91a06.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1364818 5' Similar to SW:FBP HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
ACCESSION AI019594.1 GI:3233930
VERSION AI019594
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,N. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

```

Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGS Consortium (info@image.lnl.gov) for further information.
 MGI:1898038

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.

FEATURES

source
 1. .46
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:1364818"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares_mammary_gland_NbMMG"
 /note="Organ: mammary gland; Vector: pT7T3D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo (dT) primer [5',
 TGTACCAATCTGAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT7T3 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."

ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 46;
 Best Local Similarity 76.2%; Pred. No. 3e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 AGCGGAGTGTGGCAGGACG 22
 ||||| ||||| ||||| |||||
 Db 30 AGCGGAGGAGGACCCCG 10

RESULT 8

CT017058
 LOCUS 28 bp DNA linear GSS 09-AUG-2005
 DEFINITION KBrH128N12 genomic clone, KBrH (HindIII) BAC library Brassica rapa
 subsp. pekinensis, genomic survey sequence.
 CT017058
 ACCESSION
 VERSION
 CT017058.1 GI:71469781
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica rapa subsp. pekinensis
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 Viehoveer,P., Holtgraewe,D. and Weishaar,B.
 BAC end sequences of Brassica rapa
 JOURNAL Unpublished
 2 (bases 1 to 28)
 REFERENCE Li,Y. and Weishaar,B.
 AUTHORS Direct Submission
 TITLE Submitted (09-AUG-2005) Weishaar B., Bielefeld University,
 JOURNAL Institute for Genome Research, Universitaetsstrasse 25, D-33594
 Bielefeld, Germany

COMMENT

Contact: Bernd Weishaar
 Bielefeld University, Institute for Genome Research
 Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:
 bernd.weishaar@uni-bielefeld.de
 BAC end sequences of Brassica rapa BAC clone KBrH128N12; generated
 as contribution to the 'Multinational Brassica rapa Sequencing
 Project' Seq primer: ml3f TGTAAGGAGCGGCAGT

Class: BAC ends.

FEATURES

source
 1. .28
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /strain="Chiifu type 401-42"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrH128N12"
 /clone_lib="KBrH, Brassica rapa HindIII BAC library
 GF-SCF-1002, Vector: pCUGIBac1"
 /lab_host="E.coli DH10B"

ORIGIN

Query Match 53.3%; Score 12.8; DB 11; Length 28;
 Best Local Similarity 70.8%; Pred. No. 3.5e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGTGGCAAGCAGC 24
 ||||| ||||| ||||| |||||
 Db 1 CAGCAGAGAGAGACCAACAGGC 24

RESULT 9

AZ776950
 LOCUS 33 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0011H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0011H04 F, genomic survey sequence.
 AZ776950
 ACCESSION
 VERSION
 AZ776950.1 GI:12905041
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
 1 (bases 1 to 33)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

Plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0011 row: H column: 04
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 33.

FEATURES

source

1. .33
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0011H04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 33;
Best Local Similarity 87.5%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCA 20
||||| ||||| |||||
Db 18 GGAGTGAGGCGCAGCA 33

RESULT 10

AZ840176/c
LOCUS
DEFINITION
2M0136B09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0136B09 R, genomic survey sequence.

ACCESSION
AZ840176
VERSION
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 49)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0136 row: B column: 09

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 49.

FEATURES

source
Location/Qualifiers

1..49
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0136B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 49;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCA 20
||||| ||||| |||||
Db 20 GGTGTGGTGGCAAGCA 5

RESULT 11

DR49P1S/c
LOCUS
DEFINITION
49 bp DNA linear GSS 22-NOV-2002
Danio rerio genomic clone DKEY-49P1, genomic survey sequence.

ACCESSION
AL981974.1
VERSION
GI:25187155

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

Humphray, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 49P1. 49P1 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source
Location/Qualifiers

1..49
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-49P1"
/tissue_type="Testis"
/note="Vector pindigoBAC-536"

ORIGIN

Query Match 53.3%; Score 12.8; DB 11; Length 49;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TGATGGCAGCAGCAC 24
||||| ||||| |||||
Db 44 TGATGAGAGCAGCAC 29

RESULT 12

AU104990
LOCUS
DEFINITION
50 bp mRNA linear EST 28-JAN-2004
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC07124, mRNA sequence.

ACCESSION

AU104990


```

VERSION      AU104990.1  GI:13554511
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES     Location/Qualifiers
             source
              1..50
              /organism="Homo sapiens"
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              /db_xref="taxon:9606"
              /clone="HRC07124"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CGGAGTGATGGCAGC 19
        ||||| ||||| ||||| ||
Db      16  CGGAGAGATGGCAGC 31

RESULT 13
AU104991
LOCUS     AU104991      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AU104991 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC09325, mRNA sequence.
ACCESSION AU104991
VERSION   AU104991.1  GI:13554512
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES     Location/Qualifiers
             source
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HRC07124"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CGGAGTGATGGCAGC 19
        ||||| ||||| ||||| ||
Db      16  CGGAGAGATGGCAGC 31

RESULT 15
AU104992
LOCUS     AU104992      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AU104992 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC11771, mRNA sequence.
ACCESSION AU104992
VERSION   AU104992.1  GI:13554513
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES     Location/Qualifiers
             source
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HRC11771"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CGGAGTGATGGCAGC 19
        ||||| ||||| ||||| ||
Db      10  CGGAGATGGCAGC 25

RESULT 15
CA913527/c
LOCUS     CA913527      42 bp      mRNA      linear      EST 27-DEC-2002
DEFINITION PCS01597X5 Scarlet Runner Bean Susceptor Region Triplex2 Phaseolus
            coccineus cDNA 5' similar to sal85c10.y1 Gm-c1063 Glycine max cDNA,
            mRNA sequence.
ACCESSION CA913527
VERSION   CA913527.1  GI:27400519
```

```

source
  1..50
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="HRC09325"
  /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CGGAGTGATGGCAGC 19
        ||||| ||||| ||||| ||
Db      10  CGGAGATGGCAGC 25

RESULT 14
AU104992
LOCUS     AU104992      50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AU104992 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC11771, mRNA sequence.
ACCESSION AU104992
VERSION   AU104992.1  GI:13554513
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yuuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
FEATURES     Location/Qualifiers
             source
              1..50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="HRC11771"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  CGGAGTGATGGCAGC 19
        ||||| ||||| ||||| ||
Db      10  CGGAGTTATGGCAGC 25

RESULT 15
CA913527/c
LOCUS     CA913527      42 bp      mRNA      linear      EST 27-DEC-2002
DEFINITION PCS01597X5 Scarlet Runner Bean Susceptor Region Triplex2 Phaseolus
            coccineus cDNA 5' similar to sal85c10.y1 Gm-c1063 Glycine max cDNA,
            mRNA sequence.
ACCESSION CA913527
VERSION   CA913527.1  GI:27400519
```

KEYWORDS
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eutrosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

REFERENCE
AUTHORS 1 (bases 1 to 42)
 Bui, A.Q., Le, B.H., Meterings, K., Bi, Y.-P., Choi, J.-S., McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and Goldberg, R.B.
TITLE Gene Activity in Different Regions of a Post-Fertilization Plant Embryo by EST Analysis
JOURNAL Unpublished (2002)
COMMENT Contact: Goldberg, R.B.
 Department of Molecular, Cell, & Developmental Biology
 University of California, Los Angeles
 621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
 Tel: 310 825 3270
 Fax: 310 825 8201
 Email: bobg@ucla.edu
 Seq primer: 5' Triplex
 POLYA=No.

FEATURES
 source
 Location/Qualifiers
 1..42
 /organism="Phaseolus coccineus"
 /mol_type="mRNA"
 /cultivar="Hammond's Dwarf Scarlet"
 /db_xref="taxon:3886"
 /dev_stage="6-days post-pollination"
 /clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
 /note="Organ: Suspensor Region of Globular-Stage Embryos; Vector: Triplex2; Site: 1: SfiIA; Site 2: SfiIB; Suspensor regions were micro-dissected from globular-stage embryos six days after pollination from greenhouse-grown plants [Meterings et al., Plant Cell 13, 2409-2425 (2001)]. Double-stranded cDNA was synthesized from suspensor mRNA using the SMART cDNA Library Construction Kit according to the manufacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the SfiI restriction site of the lambda Triplex2 vector (Clontech), and the recombinant cDNAs were transformed into E. coli XL1-Blue cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda Triplex2 recombinants in E. coli EM25-8 cells (Clontech)."

ORIGIN
 Query Match 52.5%; Score 12.6; DB 6; Length 42;
 Best Local Similarity 78.9%; Pred. NO. 4.5e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAAGC 19
 |||||||
 DB 25 CATCGGAGTCATGGCAGC 7

RESULT 16
LOCUS AU108033
DEFINITION AU108033 Sugano Homo sapiens cDNA library EST 28-JAN-2004
 ZRVC6413, mRNA sequence.
ACCESSION AU108033
VERSION AU108033.1 GI:13557555
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

TITLE
JOURNAL Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
PUBMED Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMO Rep. 2 (5), 388-393 (2001)
COMMENT 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ZRVC6413"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
 Query Match 52.5%; Score 12.6; DB 1; Length 50;
 Best Local Similarity 78.9%; Pred. NO. 4.6e+05;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CAGCGGAGTGATGGCAAGC 19
 |||||||
 DB 30 CAGCGGAGTCCTGAGAAGC 48

RESULT 17
LOCUS AZ2823791
DEFINITION AZ2823791 23 bp DNA linear GSS 20-FEB-2001
 2M0098H06F Mouse 10kb plasmid UGCLIB library Mus musculus genomic clone UGUC2M0098H06 F, genomic survey sequence.
ACCESSION AZ2823791
VERSION AZ2823791.1 GI:12993699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0098 row: H column: 06
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
FEATURES
 source
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGUC2M0098H06"

```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCLIM library"
/notes="Vector: pMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [G1/4732114|GB|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

```

Query Match      51.7%; Score 12.4; DB 9; Length 23;
Best Local Similarity 72.7%; Pred. No. 5.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 CAGCGAGTGATGGCAAGCAGC 22
    ||| ||| ||| ||| ||| |||
DB 22 CAGATAAGGTATGTCAAGCAGC 1

```

RESULT 18

```

A1443308/c
LOCUS
DEFINITION
  sa30a08.x1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
  Gm-cl004-763 3' similar to TR:Q39827 Q39827 ARGININE DECARBOXYLASE.
  ; mRNA sequence.

```

ACCESSION

```

A1443308
A1443308.1 GI:4302261
EST.

```

KEYWORDS

```

Glycine max (soybean)

```

ORGANISM

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

```

REFERENCE

```

1 (bases 1 to 31)
Shoemaker,R., Keim,P., Vodkin,L., Erpelnding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

```

TITLE

JOURNAL

COMMENT

```

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. Trace
considered overall poor quality possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
4163; email: info@biogeneticservices.com)
Seq primer: -400P from Gibco
High quality sequence stop: 1
POLYA=No.

```

FEATURES

source

Location/Qualifiers

```

1..31
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-783"
/tissue_type="root"
/lab host="XL10-Gold"
/clone lib="Gm-cl004"
/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #20401) was used to synthesize the
cDNA. First- strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
[GAAGAGAGAGAGAGAGAGACTGTCTCGAG(T)-18]. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adaptors,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoBRL Life
Technologies' cDNA size fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) that had been
digested with EcoRI and XhoI, and phosphorylated. Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n+15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Keim & Virginia H. Coryell,
Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.keim@nau.edu,
virginia.coryell@nau.edu"

```

ORIGIN

```

Query Match      51.7%; Score 12.4; DB 1; Length 31;
Best Local Similarity 72.7%; Pred. No. 5.3e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 3 GCGGAGTGATGGCAAGCAGCAGC 24
    ||| ||| ||| ||| ||| |||
DB 26 GCAGAGATGATGTCAACCCAGC 5

```

RESULT 19

LOCUS

DEFINITION

```

BF347447
602020763F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156238
S., mRNA sequence.

```

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

```

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

1 (bases 1 to 37)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM9428 row: n column: 15
High quality sequence stop: 37.
Location/Qualifiers
1. .37

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4156238"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn67"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 51.7%; Score 12.4; DB 2; Length 37;
Best Local Similarity 72.7%; Pred. No. 5.5e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AGCGAGTGATGGCAAGCAGCA 23
|||||
Db 35 AGTGTGGGATTACAGCAGCA 14
|||||

RESULT 20
BH620252/c
LOCUS BH620252 44 bp DNA linear GSS 30-JAN-2002
DEFINITION 1007061G07.2EL_v1 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence.

ACCESSION BH620252
VERSION BH620252.1 GI:18431908
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 44)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon

AUTHORS Walbot V.
TITLE Unpublished (2001)
JOURNAL Department of Biological Sciences
COMMENT Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007061 column: 18
Class: transposon-tagged.

FEATURES
source
Location/Qualifiers
1. .44
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pluscript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 51.7%; Score 12.4; DB 9; Length 44;
Best Local Similarity 72.7%; Pred. No. 5.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGGCAAGCAGCAG 24
|||||
Db 22 GCGGAGGCACGGAAAGACAC 1
|||||

RESULT 21
BJ032969/c
LOCUS BJ032969 32 bp mRNA linear EST 26-SEP-2003
DEFINITION laevis cDNA clone XL019F12 5', mRNA sequence.

ACCESSION BJ032969
VERSION BJ032969.1 GI:17391810
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 32)
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute Of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
<http://xenopus.nibb.ac.jp>.

FEATURES
source
Location/Qualifiers
1. .32
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL019F12"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula library"

ORIGIN
Query Match 50.8%; Score 12.2; DB 3; Length 32;
Best Local Similarity 70.0%; Pred. No. 6.6e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GCGGAGTGATGGCAAGCAGCA 23
|||||
Db 22 GCGGAGTNCNGNCATGCATGA 3
|||||

RESULT 22
CZ472229
LOCUS CZ472229 33 bp DNA linear GSS 29-APR-2005
DEFINITION d01430-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element, genomic survey sequence.

```

ACCESSION      C2472229
VERSION        C2472229.1  GI:62966242
KEYWORDS
SOURCE
ORGANISM       Drosophila melanogaster (fruit fly)
               Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 33)
AUTHORS        Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
               Singh,C.M., Buchholz,R., Densky,M., Fawcett,R., Francis-Lang,H.L.,
               Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
               Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
               Laufer,A., Mazotta,V., Smith,R.D., Stevens,L.M., Stuber,C.,
               Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
               Swimmer,C., Kopcynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
TITLE          A complementary transposon tool kit for Drosophila melanogaster
               using P and piggyBac
JOURNAL        Nat. Genet. 36 (3), 283-287 (2004)
PUBMED         14981521
COMMENT        Contact: Roger A Hoskins
               Berkeley Drosophila Genome Project
               Lawrence Berkeley National Laboratory
               Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
               Tel: 510 486 4015
               Fax: 510 486 6798
               Email: RHoskins@lbl.gov
               Sequence recovery method was inverse PCR.
               Sequence orientation is forward strand relative to 5' end of P
               element.
               The P element insertion position is 1 in the 33 bases. This
               insertion position refers to the first base of the 8 base target
               recognition sequence.
               Class: transposon insertion site.
FEATURES       Location/Qualifiers
               1..33
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /strain="isogenic w- strain"
               /db_xref="taxon:7227"
               /clone_lib="Exelixis P element XP insertions"
               /notes="Vector: P element XP (GenBank accession number
               AV515149); An isogenic w- Drosophila melanogaster strain
               was mutagenized by remobilization of transposable
               elements. For the P element XP, we selected an easily
               mobilized ammunition element among inserts hopped onto the
               Binsyncy balancer. New insertions were collected in vials
               from dysgenic females using the standard chromosomal
               source of transposase, delta2-3. All lines were mapped to
               a chromosome by standard genetic methods, examined for
               homozygous viability and used for recovery of flanking
               genomic sequence by inverse PCR."
ORIGIN
Query Match      50.8%; Score 12.2; DB 10; Length 33;
Best Local Similarity 82.4%; Pred. No. 6.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGTGTCGCAAGCAC 21
    ||||| ||||| |||||
Db 1 GGAGAGATTACAGCAC 17

RESULT 23
AV833104
LOCUS          AV833104 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION     vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
               clone bags11124, mRNA sequence.
ACCESSION      AV833104
VERSION        AV833104.1  GI:14525193
KEYWORDS
SOURCE         Hordeum vulgare subsp. vulgare

Query Match      50.8%; Score 12.2; DB 10; Length 33;
Best Local Similarity 82.4%; Pred. No. 6.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGTGTCGCAAGCAC 21
    ||||| ||||| |||||
Db 1 GGAGAGATTACAGCAC 17

RESULT 24
AV833196/c
LOCUS          AV833196/c
DEFINITION     1M0584P01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC1M0584P01 R, genomic survey sequence.
ACCESSION      AZ773196
VERSION        AZ773196.1  GI:12897306
KEYWORDS
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 38)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islami,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0584 row: P column: 01
               Seq primer: CACACGGAACACGCTATGACC
               Class: plasmid ends

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```

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 44;
Best Local Similarity 82.4%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAC 21
    ||||| ||||| ||||| ||
Db 7 GGAGGGATGTCAGGCAC 23
    ||||| ||||| ||||| ||

RESULT 27
AV947544 47 bp mRNA linear EST 14-MAR-2002
LOCUS
DEFINITION AV947544 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad01b12 5', mRNA sequence.
ACCESSION AV947544
VERSION AV947544.1 GI:19425303
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..47
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad01b12"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 47;
Best Local Similarity 82.4%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGGATGTGATGCCAA 17
    ||||| ||||| ||||| ||
Db 13 CAGCGGTGTGTGCTAA 29
    ||||| ||||| ||||| ||

RESULT 28
BH863108 42 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_093178 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093178, genomic survey sequence.
ACCESSION BH863108
VERSION BH863108.1 GI:22098437
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
Location/Qualifiers
1..42

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093178"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGAC 24
    ||||| ||||| ||||| ||
Db 15 GGAGTGATTTCAAAACTAC 34
    ||||| ||||| ||||| ||

RESULT 29
BH863111 42 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_093187 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093187, genomic survey sequence.
ACCESSION BH863111
VERSION BH863111.1 GI:22098440
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
Location/Qualifiers
1..42

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093178"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

```

```

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
Location/Qualifiers
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093178"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGAC 24
    ||||| ||||| ||||| ||
Db 15 GGAGTGATTTCAAAACTAC 34
    ||||| ||||| ||||| ||

RESULT 29
BH863111 42 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_093187 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093187, genomic survey sequence.
ACCESSION BH863111
VERSION BH863111.1 GI:22098440
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
Location/Qualifiers
1..42

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093178"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093197"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24
||||| ||| |||
Db 15 GGAGTGATTCAAAACTAC 34

RESULT 30
BH863117
LOCUS
DEFINITION SALK_093195 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093195, genomic survey sequence.

ACCESSION BH863117
VERSION BH863117.1 GI:22098446
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 42)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.

FEATURES

source
1..42
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093195"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24
||||| ||| |||
Db 15 GGAGTGATTCAAAACTAC 34

RESULT 31
BH863151
LOCUS
DEFINITION SALK_093283 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093283, genomic survey sequence.

ACCESSION BH863151
VERSION BH863151.1 GI:22098480
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 42)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.

FEATURES
source
1..42
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093283"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24
||||| ||| |||
Db 15 GGAGTGATTCAAAACTAC 34

RESULT 32
AQ902826/c
LOCUS
DEFINITION K071087-T7 Library RPII,3-5 Human PAC Homo sapiens genomic clone
RPII704K071087, genomic survey sequence.

ACCESSION AQ902826
VERSION AQ902826.1 GI:7673877
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.


```

Query Match          50.0%; Score 12; DB 9; Length 49;
Best Local Similarity 75.0%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGATGGCAAGCAC 21
Db 26 AGCGGAGAGAGCTAGGCC 45

RESULT 35
AJ600111
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
500C09 genomic survey sequence.
ACCESSION
AJ600111.1 GI:37949739
VERSION
GSS; right border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1
  Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
  Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
  Lepiniec,E., Caboche,M. and Lecharny,A.
  T-DNA integration into the Arabidopsis genome depends on sequences
  of pre-insertion sites
  EMBO Rep. 3 (12), 1152-1157 (2002)
  12446565
REFERENCE
2 (bases 1 to 50)
Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
  Location/Qualifiers
    1..50
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /db_xref="taxon:3702"
      /clone="500C09"
      /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
      /ecotype="Wassilewskija"
  misc_feature
    1..50
      /note="T-DNA flanking sequence
      right border"
ORIGIN
  Query Match          50.0%; Score 12; DB 10; Length 50;
  Best Local Similarity 75.0%; Pred. No. 8.7e+05;
  Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCA 20
Db 18 CAACGGAGTGATGATAGGAA 37

RESULT 36
CR086418
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and

```

```

chromosome engineering clone MHPp182e10, genomic survey sequence.
CR086418
VERSION
GI:49820010
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 50)
  Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
  Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
  Rogers,J. and Bradley,A.
  Direct Submission
  Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
  CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
  source
    1..50
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10090"
      /clone="MHPp182e10"
      /clone_lib="MHPP"
ORIGIN
  Query Match          50.0%; Score 12; DB 11; Length 50;
  Best Local Similarity 75.0%; Pred. No. 8.7e+05;
  Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCAAGCACGAC 24
Db 32 GGATTAAGGATGCACAC 13

RESULT 37
CZ473756/c
LOCUS
DEFINITION
d04146-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic sequence recovered from 3' end of P element,
genomic survey sequence.
ACCESSION
CZ473756
VERSION
CZ473756.1 GI:62967769
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 30)
  Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
  Singh,C.M., Buchholz,R., Demaky,M., Fawcett,R., Francis-Lang,H.L.,
  Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
  Greer,K., Hatzouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
  Lauffer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
  Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
  Swimmer,C., Koczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
  A complementary transposon tool kit for Drosophila melanogaster
  using P and piggyBac
  Nat. Genet. 36 (3), 283-287 (2004)
  14981521
  Contact: Roger A Hoskins
  Berkeley Drosophila Genome Project
  Lawrence Berkeley National Laboratory
  Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
  Tel: 510 486 4015
  Fax: 510 486 6798
  Email: RHoskins@lbl.gov
  Sequence recovery method was inverse PCR.
  Sequence orientation is forward strand relative to 5' end of P
  element.
  The P element insertion position is 1 in the 30 bases. This
  insertion position refers to the first base of the 8 base target
  recognition sequence.

```

FEATURES
source

Class: transposon insertion site.
Location/Qualifiers
1. .30
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis p element XP insertions"
/note="Vector: P element XP (Genbank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amputation element among inserts hopped onto the Binsyncy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 49.2%; Score 11.8; DB 10; Length 30;
Best Local Similarity 86.7%; Pred. No. 1e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCG 15
|| ||||| |||||
Db 21 CACCGGAGTGAGGC 7

RESULT 38
AZ821223/c
LOCUS
DEFINITION
2M0093G24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0093G24 R, genomic survey sequence.

ACCESSION
AZ821223
VERSION
GSS.
SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: G column: 24
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.

FEATURES
source

1. .40
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0093G24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.2%; Score 11.8; DB 9; Length 40;
Best Local Similarity 69.6%; Pred. No. 1e+06;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGAAGCAGCA 23
|| ||||| ||||| |||||
Db 23 CAGTGGAGTTTGAGCATGATGA 1

RESULT 39
AZ386728/c

LOCUS
DEFINITION
1M0145C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145C20 R, genomic survey sequence.

ACCESSION
AZ386728
VERSION
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 20
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.

FEATURES
source

1. .41
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145C20"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match	49.2%;	Score 11.8;	DB 9;	Length 41;
Best Local Similarity	69.6%;	Pred. No. 1e+06;		
Matches	16;	Conservative	0;	Mismatches 7; Indels 0; Gaps 0;

Qy	1	CAGCGGAGTGATGGCAAGCAGCA 23
Db	35	CTGCAGCAAGATGGCAAGACCA 13

RESULT 40

AI497819/c

LOCUS

DEFINITION

tm89g04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165334 3'
similar to SW:WASP MOUSE P70315 WISKOTT-ALDRICH SYNDROME PROTEIN
HOMOLOG ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Trace considered overall poor quality
Insert Length: 1418 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

Search completed: December 13, 2005, 15:51:21
Job time : 2988 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 11:03:03 ; Search time 368.5 Seconds
(without alignments)
434.064 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcgagtgatggaagcagcagc 24

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	14	ADZ75765 Human ind
2	18.2	75.8	37	4	ABK05395 Human NOG
3	17.2	71.7	37	4	Aah96727 Human Chk
4	17.2	71.7	37	5	ADV17621 Human PLN
5	16.8	70.0	36	5	ADU94766 Human TER
6	16.6	69.2	37	4	ABK05358 Human NOG
7	16.6	69.2	37	5	ADV47962 HBV G-cle
8	16.6	69.2	37	5	ADV04075 Human BAC
9	16.6	69.2	37	5	ADV04149 Human BAC
10	16.6	69.2	37	5	ADV04093 Human BAC
11	16.6	69.2	37	5	ADV17630 Human PLN
12	16.6	69.2	37	5	ADV04128 Human BAC
13	16.6	69.2	37	6	ABK59131 Human CLC
14	16.6	69.2	37	8	ACD53318 HBV G-cle
15	16.6	69.2	37	12	ADM61879 Hepatitis
16	16.4	68.3	45	10	ADC33588 Human loc
17	16.2	67.5	32	3	Acd00496 Clone cgm
18	16.2	67.5	37	4	ABK05366 Human NOG
19	16.2	67.5	37	5	ADV47946 HBV G-cle

20	16.2	67.5	37	6	ABK20721	Abk20721 Human ERG
21	16.2	67.5	37	8	ACD53251	AcD53251 HBV G-cle
22	16.2	67.5	37	12	ADM61863	Adm61863 Hepatitis
23	16	66.7	18	4	AaH47991	AaH47991 Human ind
24	15.8	65.8	36	5	ADU85578	AdU85578 Anti huma
25	15.8	65.8	36	5	ADU94721	AdU94721 Human TER
26	15.8	65.8	36	5	ADU94968	AdU94968 Human TER
27	15.8	65.8	36	5	ADU94463	AdU94463 Human TER
28	15.8	65.8	36	5	ADM90363	Adm90363 Human PTP
29	15.8	65.8	36	5	ADU85545	AdU85545 Human Met
30	15.8	65.8	36	5	ADM90361	Adm90361 Human PTP
31	15.8	65.8	36	5	ADU94468	AdU94468 Human TER
32	15.8	65.8	37	4	AaH96713	AaH96713 Human Chk
33	15.8	65.8	37	4	ABK05427	Abk05427 Human NOG
34	15.8	65.8	37	4	ABK08475	Abk08475 Human CD2
35	15.8	65.8	37	6	ABK59121	Abk59121 Human CLC
36	15.8	65.8	37	6	ABK59178	Abk59178 Human CLC
37	15.8	65.8	37	6	ABK59155	Abk59155 Human CLC
38	15.6	65.0	37	4	ABK05394	Abk05394 Human NOG
39	15.6	65.0	37	4	ABK05401	Abk05401 Human NOG
40	15.6	65.0	37	4	ABK05385	Abk05385 Human NOG
41	15.6	65.0	37	5	ADV04196	Adv04196 Human BAC
42	15.6	65.0	37	5	ADV48009	Adv48009 HBV G-cle
43	15.6	65.0	37	8	ACD53331	AcD53331 HBV G-cle
44	15.6	65.0	37	12	ADM61892	Adm61892 Hepatitis
45	15.2	63.3	36	5	ADM90417	Adm90417 Human PTP

ALIGNMENTS

RESULT 1

ADZ75765
ID ADZ75765 standard; DNA; 24 BP.

XX AC ADZ75765;

XX XX 28-JUL-2005 (first entry)

XX DE Human inducible nitric oxide synthase gene exon 7 forward PCR primer.

XX KW ss; PCR; high altitude pulmonary edema; pulmonary edema;

XX KW respiratory-gen.; respiratory disease; SNP detection; allelic variation;

XX KW primer; exon.

XX OS Homo sapiens.

XX XX US2005106573-A1.

XX XX 19-MAY-2005.

XX PD 13-NOV-2003; 2003US-00713137.

XX PF 13-NOV-2003; 2003US-00713137.

XX XX 13-NOV-2003; 2003US-00713137.

XX XX (COUN-) COUNCIL SCI & IND RES INDIA.

XX XX Pasha AQM, Ahsan A;

XX XX WPI; 2005-384299/39.

XX PT Detecting predisposition to high altitude pulmonary edema (HAPE) by

XX PT amplifying intron 7 of human inducible nitric oxide synthase gene; and

XX PT predicting and analyzing differences in the distribution of allelic

XX PS Claim 6; SEQ ID NO 2; 13pp; English.

XX CC The invention relates to a novel method for detecting predisposition to

XX CC high altitude pulmonary edema (HAPE). The method comprises amplifying

XX CC intron 7 of the human inducible nitric oxide synthase (iNOS) gene

XX CC (ADZ75764) by designing and synthesizing forward and reverse

XX CC oligonucleotide primers (ADZ75765+ADZ75766), and predicting and

CC statistically analyzing differences in the distribution of the allelic
CC variants in the populations, where GG genotype at 19480 position are at
CC low risk of HAPE, and AA genotype at 19480 position are at high risk of
CC HAPE. The present sequence represents the forward oligonucleotide primer
CC of the invention.
XX
SQ Sequence 24 BP; 7 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGAC 24
|||||
Db 1 CAGCGAGTGATGGCAAGCAGAC 24

RESULT 2
ABK05395
ID ABK05395 standard; RNA; 37 BP.
XX
AC ABK05395;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO G-Cleaver substrate sequence #58.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 89; Page 92; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NOGO sequence
XX
SQ Sequence 37 BP; 10 A; 8 C; 12 G; 0 T; 7 U; 0 Other;

Query Match 75.8%; Score 18.2; DB 4; Length 37;
Best Local Similarity 78.3%; Pred. No. 1.1e+02;
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCA 23
|||||
Db 1 CAGAGGAGUGAUGCAUGCACUA 23

RESULT 3
AAH96727
ID AAH96727 standard; RNA; 37 BP.
XX
AC AAH96727;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human Chk1 ribozyme SEQ ID NO: 2152.
XX
KW Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
KW RNA cleavage; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157206-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003504.
XX
PR 03-FEB-2000; 2000US-0179983P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (FATT/) FATTAEY A R.
XX
PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
XX
DR WPI; 2001-496922/54.
XX
PT Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
PT molecules, which downregulates expression of a checkpoint kinase-1 gene,
PT useful for treating colorectal, lung, breast or prostate cancers.

XX Claim 5; Page 68; 115pp; English.

XX The present invention provides nucleic acid molecules capable of

XX downregulating the expression of the human checkpoint kinase-1 (Chk1)

XX gene. These may be antisense or ribozyme sequences, and are useful in the

XX treatment of diseases associated with conditions affected by Chk1 levels,

XX including cancer. The present sequence is an oligonucleotide described in

XX the exemplification of the invention

XX Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;

XX

Query Match 71.7%; Score 17.2; DB 4; Length 37;

Best Local Similarity 77.3%; Pred. No. 3.1e+02;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGTGTCGACAGCACGA 23

DB 2 AGAGGAGUGAUGGCAUGCACUA 23

RESULT 4

ADV17621

ID ADV17621 standard; RNA; 37 BP.

XX ADV17621;

XX

XX 10-FEB-2005 (first entry)

XX

XX Human PLN G-cleaver ribozyme sequence #9.

XX

XX Enzymatic nucleic acid molecule; gene expression; down regulation;

XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;

XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;

XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;

XX C-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;

XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;

XX amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;

XX diabetes; obesity; cardiac disease; heart disease; age-related disease;

XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

XX ss.

XX Homo sapiens.

XX

XX WO200116312-A2.

XX

XX 08-MAR-2001.

XX

XX 30-AUG-2000; 2000WO-US023998.

XX

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 29-DEC-1999; 99US-0173612P.

XX 30-DEC-1999; 99US-00476387.

XX 04-FEB-2000; 2000US-00498824.

XX 20-MAR-2000; 2000US-00531025.

XX 14-APR-2000; 2000US-0197769P.

XX 23-MAY-2000; 2000US-00578223.

XX 09-AUG-2000; 2000US-00636385.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX

XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

XX Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX

XX WPI; 2001-244406/25.

XX

PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules

PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

PT obesity and heart disease.

XX Example 5; Page 428; 717pp; English.

XX

XX The present invention relates to the use of enzymatic nucleic acid

XX molecules (e.g. ribozymes) to modulate gene expression. The invention

XX also methods for their use to down regulate or inhibit the expression of

XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine

XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor

XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic

XX nucleic acid molecules used to inhibit the expression of the said genes

XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,

XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful

XX for treating cancer, in particular breast cancer, Alzheimer's disease,

XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related

XX diseases, hepatitis B infections, and hepatitis and hepatocellular

XX carcinoma. The enzymatic nucleic acid molecules can also be used as

XX diagnostic tools to examine genetic drift and mutations within diseased

XX cells and to detect the presence of specific RNA in a cell. The present

XX sequence represents a ribozyme used in the examples of the present

XX invention. Note: Some SEQ ID Nos are repeated more than once in the

XX specification, but these have different sequences associated with them.

XX

XX Sequence 37 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 0 Other;

XX

Query Match 71.7%; Score 17.2; DB 5; Length 37;

Best Local Similarity 77.3%; Pred. No. 3.1e+02;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGTGTCGACAGCACGA 23

DB 2 AGCUGAGUGAUGGCAUGCACUA 23

RESULT 5

ADU94766

ID ADU94766 standard; RNA; 36 BP.

XX ADU94766;

XX

XX 10-FEB-2005 (first entry)

XX

XX Human TERT G-cleaver ribozyme sequence #157.

XX

XX Enzymatic nucleic acid molecule; gene expression; down regulation;

XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;

XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;

XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;

XX C-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;

XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;

XX amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;

XX diabetes; obesity; cardiac disease; heart disease; age-related disease;

XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

XX ss.

XX Homo sapiens.

XX

XX WO200116312-A2.

XX

XX 08-MAR-2001.

XX

XX 30-AUG-2000; 2000WO-US023998.

XX

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 29-DEC-1999; 99US-0173612P.

XX 30-DEC-1999; 99US-00476387.

XX 04-FEB-2000; 2000US-00498824.

XX 20-MAR-2000; 2000US-00531025.

XX 14-APR-2000; 2000US-0197769P.

XX 23-MAY-2000; 2000US-00578223.

XX 09-AUG-2000; 2000US-00636385.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX

XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

XX Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX

XX WPI; 2001-244406/25.

XX

PR 29-DEC-1999; 99US-00474432.
 PR 29-DEC-1999; 99US-0173612P.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-00531025.
 PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578223.
 PR 09-AUG-2000; 2000US-00636385.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
 PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
 DR WPI; 2001-244406/25.
 XX
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.
 PT
 XX Example 1; Page 304; 717pp; English.
 PS
 CC The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zynzyme, and/or DNAzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.
 XX
 SQ Sequence 36 BP; 8 A; 10 C; 12 G; 0 T; 6 U; 0 Other;
 Query Match 70.0%; Score 16.8; DB 5; Length 36;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGGAGTGATGGCAACGACA 23
 |||||:|||||
 Db 1 CGGAGUGAUGGCAUGACUA 20
 RESULT 6
 ABK05358
 ID ABK05358 standard; RNA; 37 BP.
 XX
 AC ABK05358;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 XX Human NOGO G-Cleaver substrate sequence #21.
 DE
 XX Human; sg; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN 16-AUG-2001.
 PD
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B W.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 89; Page 92; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 37 BP; 5 A; 10 C; 17 G; 0 T; 5 U; 0 Other;
 Query Match 69.2%; Score 16.6; DB 4; Length 37;
 Best Local Similarity 73.9%; Pred. No. 6e+02;
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGCACGA 23
 ||||| :|||:|||||
 Db 1 CAGGGGGGUGAUGGCAUGCACUA 23

RESULT 7
 ADV47962
 ID ADV47962 standard; RNA; 37 BP.
 XX
 AC ADV47962;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE HBV G-cleaver ribozyme sequence #57.
 XX
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
 KW
 OS Hepatitis B virus.
 XX
 XX WO200116312-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023398.
 XX
 XX 31-AUG-1999; 99US-0151713P.
 PR 27-SEP-1999; 99US-00406643.
 PR 27-SEP-1999; 99US-0156236P.
 PR 27-SEP-1999; 99US-0156467P.
 PR 08-NOV-1999; 99US-00436430.
 PR 06-DEC-1999; 99US-0169100P.
 PR 29-DEC-1999; 99US-00474432.
 PR 29-DEC-1999; 99US-0173612P.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-00531025.
 PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578223.
 PR 09-AUG-2000; 2000US-00636385.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;
 PI Karpelesky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 XX
 DR WPI; 2001-244406/25.
 XX
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 XX obesity and heart disease.
 XX
 PS Example 6; Page 531; 717pp; English.
 XX
 XX The present invention relates to the use of enzymatic nucleic acid
 XX molecules (e.g. ribozymes) to modulate gene expression. The invention
 XX also methods for their use to down regulate or inhibit the expression of
 XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 XX nucleic acid molecules used to inhibit the expression of the said genes
 XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
 XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful

CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.
 XX
 SQ Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
 XX
 Query Match 69.2%; Score 16.6; DB 5; Length 37;
 Best Local Similarity 73.9%; Pred. No. 6e+02;
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 1 CAGCGGAGTGATGGCAGCACGA 23
 ||||| :|||:|||||
 Db 1 CAGCCUAGUGAUGGCAUGCACUA 23

RESULT 8
 ADV04075
 ID ADV04075 standard; RNA; 37 BP.
 XX
 AC ADV04075;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human BACE G-cleaver ribozyme sequence #12.
 XX
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200116312-A2.
 XX
 XX 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023398.
 XX
 XX 31-AUG-1999; 99US-0151713P.
 PR 27-SEP-1999; 99US-00406643.
 PR 27-SEP-1999; 99US-0156236P.
 PR 27-SEP-1999; 99US-0156467P.
 PR 08-NOV-1999; 99US-00436430.
 PR 06-DEC-1999; 99US-0169100P.
 PR 29-DEC-1999; 99US-00474432.
 PR 29-DEC-1999; 99US-0173612P.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-00531025.
 PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578223.
 PR 09-AUG-2000; 2000US-00636385.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;
 PI Karpelesky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 XX
 DR WPI; 2001-244406/25.
 XX

PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.

XX Example 4; Page 364; 717pp; English.

CC The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX Sequence 37 BP; 5 A; 9 C; 18 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAGCAGCA 23

Db 1 CGCGCGCGUGAUGGCAUGCAGCA 23

RESULT 9

ADV04149

ID ADV04149 standard; RNA; 37 BP.

AC ADV04149;

DT 10-FEB-2005 (first entry)

DE Human BACE G-cleaver ribozyme sequence #52.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinyne; DNzyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.

OS Homo sapiens.

XX WO200116312-A2.

PN 08-MAR-2001.

PD 30-AUG-2000; 2000WO-US023998.

PF 31-AUG-1999; 99US-0151713P.

PR 27-SEP-1999; 99US-00406643.

PR 27-SEP-1999; 99US-0156236P.

PR 27-SEP-1999; 99US-0156467P.

PR 08-NOV-1999; 99US-00436430.

PR 06-DEC-1999; 99US-0169100P.

PR 29-DEC-1999; 99US-00474432.

PR 29-DEC-1999; 99US-0173612P.

PR 04-DEC-1999; 99US-00476387.

PR 04-FEB-2000; 2000US-00498824.

PR 20-MAR-2000; 2000US-00531025.

PR 14-APR-2000; 2000US-0197769P.

PR 23-MAY-2000; 2000US-00578223.

PR 09-AUG-2000; 2000US-00636395.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A,

PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;

XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 XX obesity and heart disease.

PS Example 4; Page 365; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX Sequence 37 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAGCAGCA 23

Db 1 CAGCGCGUGAUGGCAUGCAGCA 23

RESULT 10

ADV04093

ID ADV04093 standard; RNA; 37 BP.

XX ADV04093;

XX 10-FEB-2005 (first entry)

DE Human BACE G-cleaver ribozyme sequence #30.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinyne; DNzyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;

hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

ss.

Homo sapiens.

WO200116312-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023998.

31-AUG-1999; 99US-0151713P.
27-SEP-1999; 99US-00406643.
27-SEP-1999; 99US-0156236P.
27-SEP-1999; 99US-0156467P.
08-NOV-1999; 99US-00436430.
06-DEC-1999; 99US-0169100P.
29-DEC-1999; 99US-00474432.
29-DEC-1999; 99US-0173612P.
30-DEC-1999; 99US-00476387.
04-FEB-2000; 2000US-00498824.
20-MAR-2000; 2000US-00531025.
14-APR-2000; 2000US-0197769P.
23-MAY-2000; 2000US-00578223.
09-AUG-2000; 2000US-00636385.

(RIBO-) RIBOZYME PHARM INC.

Mcswigen J, Usman N, Blatt L, Beigelman L, Burgin A;
Karpeisky A, Matulich-Adamic J, Sweedler D, Draper K, Chowrira B;
Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules
are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
obesity and heart disease.

Example 4; Page 364; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid
molecules (e.g. ribozymes) to modulate gene expression. The invention of
also methods for their use to down regulate or inhibit the expression of
genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),
presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
nucleic acid molecules used to inhibit the expression of the said genes
include hammerhead (HH), hairpin, NCH (inozyme), G-Cleaver, amberyyme,
zincyme, and/or DNazyme motifs. The methods of the invention are useful
for treating cancer, in particular breast cancer, Alzheimer's disease,
diabetes, obesity, cardiac diseases e.g. heart disease, age-related
diseases, hepatitis B infections, and hepatitis and hepatocellular
carcinoma. The enzymatic nucleic acid molecules can also be used as
diagnostic tools to examine genetic drift and mutations within diseased
cells and to detect the presence of specific RNA in a cell. The present
sequence represents a ribozyme used in the examples of the present
invention. Note: Some SEQ ID Nos are repeated more than once in the
specification, but these have different sequences associated with them.

Sequence 37 BP; 9 A; 7 C; 16 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;
Best Local Similarity 73.9%; Pred. No. 6e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCACGA 23
DB 1 CACGGGAGUAGUGCAUGCACUA 23

RESULT 11

CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX SQ Sequence 37 BP; 11 A; 8 C; 11 G; 0 T; 7 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGGCAAGCACGA 23

Db 1 CAGAGAGUGAUGGCAUGCACUA 23

RESULT 12

ADV04128

ID ADV04128 standard; RNA; 37 BP.

XX AC ADV04128;

XX DT 10-FEB-2005 (first entry)

DE Human BACE G-cleaver ribozyme sequence #31.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberyzyme; zinzyme; DNAYyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.

XX OS Homo sapiens.

XX PN WO200116312-A2.

XX PD 08-MAR-2001.

XX PF 30-AUG-2000; 2000WO-US023998.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

XX PR 27-SEP-1999; 99US-0156467P.

XX PR 08-NOV-1999; 99US-00436430.

XX PR 06-DEC-1999; 99US-0169100P.

XX PR 29-DEC-1999; 99US-00474432.

XX PR 29-DEC-1999; 99US-0173612P.

XX PR 30-DEC-1999; 99US-00476387.

XX PR 04-FEB-2000; 2000US-00498824.

XX PR 20-MAR-2000; 2000US-00531025.

XX PR 14-APR-2000; 2000US-0197769P.

XX PR 23-MAY-2000; 2000US-00578223.

XX PR 09-AUG-2000; 2000US-00636385.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (SYNT) SYNTEX USA LLC.

XX PA (THOM/) THOMPSON J.

XX PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

XX PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

XX PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX PI WPI; 2001-244406/25.

XX DR Enzymatic nucleic acid molecules able to cleave separate RNA molecules

XX PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

XX PT obesity and heart disease.

XX PS Example 4; Page 365; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
 CC zinzyme, and/or DNAYyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX SQ Sequence 37 BP; 8 A; 10 C; 14 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGGCAAGCACGA 23

Db 1 CCGCAGAGUGAUGGCAUGCACUA 23

RESULT 13

ABKS9131

ID ABKS9131 standard; RNA; 37 BP.

XX AC ABKS9131;

XX DT 02-JUL-2002 (first entry)

XX DE Human CLCA1 gene enzymatic nucleic acid #3502.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiaschmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcycteine.

XX OS Homo sapiens.

XX PN WO200211674-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (SYNT) SYNTEX USA LLC.

XX PA (THOM/) THOMPSON J.

XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX PI Grupe A;

XX PI WPI; 2002-217145/27.

XX DR Enzymatic polynucleotide that down regulates expression of chloride

XX PT channel calcium activated gene, useful for treating Chronic obstructive

XX PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX PS Claim 5; Page 87; 152pp; English.

PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
DR
XX
XX Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 4013; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
SQ
Query Match 69.2%; Score 16.6; DB 12; Length 37;
Best Local Similarity 73.9%; Pred. No. 6e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 1 CAGCGGAGTGATGGCAGCAGCA 23
DB 1 CAGCCUAGUGAUGGCAUGACUA 23
RESULT 16
ADC33588
ID ADC33588 standard; DNA; 45 BP.
XX
AC ADC33588;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human locus DYS271 30C-44A-168A variant PCR primer #4.
XX
XX Human; Y chromosome; DYS271; SNP; single nucleotide polymorphism; ss;
KW mutation detection; denaturing high performance liquid chromatography;
KW DHPLC; nitrogen containing composition; PCR; primer.
XX
XX Homo sapiens.
OS
XX US2003082557-A1.
PN
XX 01-MAY-2003.
PD
XX 29-OCT-2001; 2001US-00033104.
PF
XX 30-OCT-2000; 2000US-024436P.
PR
XX 03-JAN-2001; 2001US-0259847P.
XX
XX (TAYL/) TAYLOR P D.
PA
XX Taylor PD;
PI
XX WPI; 2003-743884/70.
DR
XX
XX Preparing a double stranded DNA fragment for mutation detection by

PT denaturing high performance liquid chromatography, comprises including
PT during hybridization composition comprising a nitrogen-containing organic
XX compound.
XX
XX Example 4; SEQ ID NO 4; 24pp; English.
XX
XX The invention relates to preparing a double stranded DNA fragment for
CC mutation detection by denaturing high performance liquid chromatography
CC (DHPLC) comprising including during the hybridisation, a nitrogen
CC containing composition (of structure detailed in the specification). The
CC double stranded DNA fragment corresponds to a wild type double stranded
CC DNA fragment having a known nucleotide sequence. The method further
CC comprises: (a) amplifying a section of the double stranded DNA fragment
CC for mutation detection by PCR using a set of primers flanking the
CC section, where at least one primer of the set incorporates a sequence
CC comprising solely GC content on the 5' end; (b) hybridising the
CC amplification product of (a) with wild type double stranded DNA
CC corresponding to the section, where a mixture comprising one or more
CC heteroduplexes is formed if the section includes a mutation; and (c)
CC including during the hybridisation, an amount of the nitrogen containing
CC composition. The composition is included to increase the amount of
CC heteroduplex DNA double stranded DNA fragment for mutation detection.
CC Also included are a product of the method above, a kit for preparing a
CC double stranded DNA for mutation detection by liquid chromatography, a
CC kit for hybridising a target nucleotide sequence with wild type DNA
CC corresponding to the target sequence, and a kit for analysing a double
CC stranded DNA for mutation detection by liquid chromatography. The method
CC is useful for preparing a double stranded DNA fragment for mutation
CC analysis, and for diagnosing a disease. The method improves the
CC resolution between heteroduplex and homoduplex peaks even for mutations
CC that are difficult to detect. The present sequence is a PCR primer used
CC to amplify variants of the human Y chromosome locus DYS271 (which
CC contains 3 single nucleotide polymorphisms) and is used to demonstrate
XX the method of the invention.
XX
XX Sequence 45 BP; 8 A; 11 C; 14 G; 7 T; 0 U; 5 Other;
SQ
Query Match 68.3%; Score 16.4; DB 10; Length 45;
Best Local Similarity 70.8%; Pred. No. 7.6e+02;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 CAGCGGAGTGATGGCAGCAGCA 24
DB 10 CAGMTGTMGTGGCATAACAGGAC 33
RESULT 17
AAD00496
ID AAD00496 standard; RNA; 32 BP.
XX
AC AAD00496;
XX
XX 29-AUG-2000 (first entry)
DT
XX
DE Clone cGMP-5 for allosteric modulation of hammerhead ribozyme by cGMP.
XX
XX Hammerhead ribozyme; molecular sensor; signalling agent; ligand; FMN;
KW flavin mononucleotide; conformational change; molecular switch; CM;
KW communication module; allosteric; sensing element; environmental;
KW agricultural; clinical; industrial; genetic control; cGMP; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1..4
FT /tag= a
FT /label= Communication_module
FT /note= "Comprises substitution mutations"
FT misc_feature 1
FT /tag= b
FT /note= "Cytosine substituted with Uracil"
FT misc_feature 3
FT /tag= c


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FT misc_feature /note= "Uracil substituted with Guanine"
FT 5..28 /tag= d
FT /note= "Corresponds to aptamer domain"
FT 29..32
FT /tag= e
FT /label= Communication module
FT /note= "Comprises substitution mutations"
FT 29
FT /tag= f
FT /note= "Adenine substituted with Uracil"
FT 30
FT /tag= g
FT /note= "Cytosine substituted with Adenine"
FT 31
FT /tag= h
FT /note= "Guanine substituted with Cytosine"
FT 32
FT /tag= i
FT /note= "Uracil substituted with Guanine"
XX
XX WO200026226-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025497.
XX
XX 03-NOV-1998; 98US-0106829P.
XX 29-MAR-1999; 99US-0126683P.
XX (UYUA ) UNIV YALE.
XX
XX Breaker RR, Soukup GA;
XX WPI; 2000-365558/31.
XX
XX Novel functional polynucleotides comprising an actuator domain, a
XX receptor domain, and a bridging domain useful for generating highly
XX specific polynucleotide sensors and as genetic control elements.
XX
XX Example 3; Fig 10A; 83pp; English.
XX
XX The patent discloses multidomain polynucleotide molecular sensors,
XX constructed using hammerhead ribozyme RNAs, comprising an actuator or
XX catalytic domain, bridging domain and receptor or aptamer domain. The
XX interaction of the receptor with a signalling agent like a ligand e.g.,
XX flavin mononucleotide (FMN) or physical signal, triggers a conformational
XX change in the bridging domain, that modulates the catalytic or reporter
XX activity of the actuator domain. It functions as a molecular switch.
XX Communication module (CM) sequences can be inserted as the bridging
XX domain, that enhances the allosteric properties. The ligand-specific
XX sensors may be used as sensing elements in clinical, agricultural,
XX industrial and environmental analyses and as genetic control or reporter
XX elements for the regulation of gene expression. The present RNA sequence
XX is the clone cGMP-5, isolated from G18' RNA population, after selective
XX amplification. It is used to study the allosteric modulation of
XX hammerhead ribozymes by cGMPs. This clone comprises mutations in the
XX aptamer domain (deletions) and communication module (substitutions)
XX
XX Sequence 32 BP; 7 A; 8 C; 11 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 67.5%; Score 16.2; DB 3; Length 32;
XX Best Local Similarity 81.0%; Pred. No. 9.1e+02;
XX Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX Q7 2 AGCGGAGTGATGGCAAGCAGC 22
XX ||||| ||||| ||||| |||||
XX Db 8 AGCGGAGCGAUGGCAGCCACG 28
XX
XX RESULT 18
XX ABRK05366
XX ID ABRK05366 standard; RNA; 37 BP.

```

```

XX ABRK05366;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NOGO G-Cleaver substrate sequence #29.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
XX musclar; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
XX DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; ankyrotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWIRRA B M.
XX
XX Blatt L, Mcswiggen J, Chowirra BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 89; Page 92; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
XX an amberszyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YCY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg2+.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the
XX presence of a divalent cation that is preferably Mg2+. Furthermore, the
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the
XX cell and treat a patient having a condition associated with the level of
XX NOGO. The treatment may further comprise the use of one or more
XX therapies. In particular, the NOGO-targeting nucleic acid may be used to

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CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NCO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NCO sequence
XX
SQ Sequence 37 BP; 6 A; 8 C; 18 G; 0 T; 5 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 4; Length 37;
Best Local Similarity 76.2%; Pred. NO. 9.2e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGTGCGCAGCACA 23
DB 3 GCGGAGUGAUGGCAUGCACUA 23

RESULT 19
ADV47946
ID ADV47946 standard; RNA; 37 BP.
AC ADV47946;
XX
DT 10-FEB-2005 (first entry)
XX
DE HBV G-cleaver ribozyme sequence #41.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyze; zinyze; DNzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.
XX
OS Hepatitis B virus.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

PT obesity and heart disease.
XX
PS Example 6; Page 531; 717pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,
CC zinyze, and/or DNzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a ribozyme used in the examples of the present
CC invention. Note: Some SEQ ID Nos are repeated more than once in the
CC specification, but these have different sequences associated with them.
XX
SQ Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 5; Length 37;
Best Local Similarity 76.2%; Pred. NO. 9.2e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGTGCGCAGCACA 23
DB 3 GCGGAGUGAUGGCAUGCACUA 23

RESULT 20
ABK20721
ID ABK20721 standard; RNA; 37 BP.
XX
AC ABK20721;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG G-cleaver ribozyme, Seq ID No 3368.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge-Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Oesler-Weber-rendu syndrome, leukaemia; osteoporosis; DNzyme; inozyme;
KW amberyze.
XX
OS Homo sapiens.
XX
PN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
XX
DR
XX

PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 PS Claim 5; Page 82; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration, verruca
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention

XX Sequence 37 BP; 7 A; 10 C; 12 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 37;
 Best Local Similarity 76.2%; Pred. No. 9.2e+02;
 Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGCCAAGCAGCA 23
 ||| |||: |||: ||| ||| |||
 Db 3 GCGUAGUGAUGGCAUGCACUA 23

RESULT 21
 ACDS3251
 ID ACDS3251 standard; RNA; 37 BP.

XX AC ACDS3251;

XX 24-SEP-2003 (first entry)

XX HBV G-cleaver sequence #41.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNase; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatitis; cytostatic;
 KW virucide; antiinflammatory; ss.

XX Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.
 XX 05-DEC-2001; 2001US-0337055P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLATY) BLATY L.

PA (MACE) MACEJAK D.

PA (MCSW) MCSWIGGEN J.

PA (MORR) MORRISSEY D.

PA (PAVC) PAVCO P.

PA (LEEP) LEE P.

PA (DRAP) DRAPER K.

PA (ROBE) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.

XX Example 1; Page 165; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNasezymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents one of the HBV ribozyme.
 CC inozyme, G-cleaver, zinzyme, DNasezyme or amberyne sequences disclosed in
 CC the present invention

XX Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 8; Length 37;

Best Local Similarity 76.2%; Pred. No. 9.2e+02;

Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGCCAAGCAGCA 23
 ||| |||: |||: ||| ||| |||

Db 3 GCGGAGUGAUGGCAUGCACUA 23

RESULT 22

ADM61863

ID ADM61863 standard; RNA; 37 BP.

XX ADM61863;

XX 03-JUN-2004 (first entry)

XX Hepatitis B virus (HBV) enzymatic nucleic acid #1455.

XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
 KW virucide; hepatotropic; antiinflammatory; cytostatic.

XX Hepatitis B virus.

XX US2004054156-A1.

XX

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PD 18-MAR-2004.
XX
PP 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
DR
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 3997; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells; for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 12; Length 37;
Best Local Similarity 76.2%; Pred. No. 9.2e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGCGACGCA 23
DB |||||:|||||
3 GCGGAGUGAUGGCAUCACUA 23

RESULT 23
ADU47991/C
ID AAH47991 standard; DNA; 18 BP.
XX
AC AAH47991;
XX
XX
DT 02-OCT-2001 (first entry)
XX
DE Human inducible NOS antisense oligonucleotide SEQ ID NO 35.
XX
KW Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
XX 2'-O-methoxyethyl; phosphorothioate; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18

```

```

FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone, 5' and 3' four
FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
FT residues in the 2'-MOE wings are 5-methylcytidines) and a
FT deoxy gap"
XX
PN WO200152902-A1.
XX
PD 26-JUL-2001.
XX
XX 15-JAN-2001; 2001WO-US001381.
XX
PR 24-JAN-2000; 2000US-00490208.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Cowseert LM;
XX WPI; 2001-465340/50.
DR
XX
PT New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischemia.
XX
PS Example 15; Page 83; 144pp; English.
XX
CC The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridise to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an
CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
XX
SQ Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGATGGCAAGCAGCAGAC 24
DB |||||:|||||
18 TGATGGCAAGCAGCAGAC 3

RESULT 24
ADU85578
ID ADU85578 standard; RNA; 36 BP.
XX
AC ADU85578;
XX
XX
DT 10-FEB-2005 (first entry)
XX
DE Anti human MetAP-2 G-cleaver ribozyme sequence #2.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-18; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;

```

KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX Homo sapiens.
XX WO200116312-A2.
PN 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023998.
XX 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX (RIBO-) RIBOZYME PHARM INC.
XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX WPT; 2001-244406/25.
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX Example 3; Page 266; 717pp; English.
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents an anti human ribozyme used in the examples of the
XX present invention. Note: Some SEQ ID Nos are repeated more than once in
XX the specification, but these have different sequences associated with
XX them.
XX Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;
XX Query Match 65.8%; Score 15.8; DB 5; Length 36;
XX Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 5 GGAGTGTGCGAUGCACGA 23
|||||:|||||

Db 2 GGAGUGAUGGCAUGCACUA 20
RESULT 25
ADU94721
ID ADU94721 standard; RNA; 36 BP.
XX AC
XX ADU94721;
XX 10-FEB-2005 (first entry)
XX Human TERT G-cleaver ribozyme sequence #143.
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HSR2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX Homo sapiens.
XX WO200116312-A2.
XX 08-MAR-2001.
XX 30-AUG-2000; 2000WO-US023998.
XX 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX (RIBO-) RIBOZYME PHARM INC.
XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX WPT; 2001-244406/25.
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX Example 1; Page 303; 717pp; English.
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,

CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

SQ Sequence 36 BP; 8 A; 9 C; 13 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;

Best Local Similarity 78.9%; Pred. No. 1.4e+03;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAGCACGA 23

DB 2 GGAGUGAUGGCAUGCACUA 20

RESULT 26

ADU94968

ID ADU94968 standard; RNA; 36 BP.

XX AC ADU94968;

XX DT 10-FEB-2005 (first entry)

XX DE Human TERT G-cleaver ribozyme sequence #266.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinczyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.

XX OS Homo sapiens.

XX PN WO200116312-A2.

XX XX 08-MAR-2001.

XX PF 30-AUG-2000; 2000WO-US023998.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

XX PR 27-SEP-1999; 99US-0156467P.

XX PR 08-NOV-1999; 99US-00436430.

XX PR 06-DEC-1999; 99US-0169100P.

XX PR 29-DEC-1999; 99US-00474432.

XX PR 29-DEC-1999; 99US-0173612P.

XX PR 30-DEC-1999; 99US-00476387.

XX PR 04-FEB-2000; 2000US-00498824.

XX PR 20-MAR-2000; 2000US-00531025.

XX PR 14-APR-2000; 2000US-0197769P.

XX PR 23-MAY-2000; 2000US-00578223.

XX PR 09-AUG-2000; 2000US-00636385.

XX XX (RIBO-) RIBOZYME PHARM INC.

XX PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

XX PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

XX PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX XX WPI; 2001-244406/25.

XX DR

XX XX

PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules

PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

XX Example 1; Page 307; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1), c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinczyme, and/or DNazyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the CC specification, but these have different sequences associated with them.

XX SQ Sequence 36 BP; 7 A; 11 C; 12 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;

Best Local Similarity 78.9%; Pred. No. 1.4e+03;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAGCACGA 23

DB 2 GGAGUGAUGGCAUGCACUA 20

RESULT 27

ADU94463

ID ADU94463 standard; RNA; 36 BP.

XX AC ADU94463;

XX DT 10-FEB-2005 (first entry)

XX DE Human TERT G-cleaver ribozyme sequence #9.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinczyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.

XX OS Homo sapiens.

XX PN WO200116312-A2.

XX PD 08-MAR-2001.

XX PF 30-AUG-2000; 2000WO-US023998.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

XX PR 27-SEP-1999; 99US-0156467P.

XX PR 08-NOV-1999; 99US-00436430.

XX PR 06-DEC-1999; 99US-0169100P.

XX PR 29-DEC-1999; 99US-00474432.

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PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 1; Page 299; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX c-erb2; neu, phospholamban; PLN, presenilin-1; ps-1; presenilin-2; HER2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberyyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX
XX Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 65.8%; Score 15.8; DB 5; Length 36;
XX Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 5 GGAGTGATGGCAGACGCA 23
XX Db 2 GGAGUGAUGGCAUGACUA 20
XX
XX RESULT 28
XX ADM90363
XX ID ADM90363 standard; RNA; 36 BP.
XX
XX AC ADM90363;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Human PTP-1B G-cleaver ribozyme sequence #110.
XX
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberyyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

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KW ss.
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 23-DEC-1999; 99US-00474432.
XX 23-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 2; Page 211; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyyme,
XX zinzyme, and/or DNzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a ribozyme used in the examples of the present
XX invention. Note: Some SEQ ID Nos are repeated more than once in the
XX specification, but these have different sequences associated with them.
XX
XX Sequence 36 BP; 8 A; 5 C; 15 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 65.8%; Score 15.8; DB 5; Length 36;
XX Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 5 GGAGTGATGGCAGACGCA 23
XX Db 2 GGAGUGAUGGCAUGACUA 20
XX
XX RESULT 29
XX ADU85545

```

ID ADU85545 standard; RNA; 36 BP.
AC ADU85545;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human MetAP-2 G-cleaver ribozyme substrate sequence #133.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
PS Example 3; Page 264; 717pp; English.

CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,
CC zinzyme, and/or DNzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present

CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
SQ Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;
XX
Query Match 65.8%; Score 15.8; DB 5; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 GGAGTGATGGCAAGCACGA 23
Db 2 GGAGUGAGGCAUGACACUA 20
||||:|||||
||||:|||||
RESULT 30
ADM90361
ID ADM90361 standard; RNA; 36 BP.
XX
AC ADM90361;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human PTP-1B G-cleaver ribozyme sequence #108.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
PS Example 2; Page 211; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX SQ Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 5 GGAGTGGATGGCAAGCAGCA 23
 |||||:|||||
 Db 2 GGAGUGAUGGCAUGCAGCA 20

RESULT 31
 ADU94468
 ID ADU94468 standard; RNA; 36 BP.
 AC ADU94468;
 XX
 XX 10-FEB-2005 (first entry)
 XX Human TERT G-cleaver ribozyme sequence #14.
 XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinyne; DNzyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.
 XX Homo sapiens.
 XX WO200116312-A2.
 XX 08-MAR-2001.
 XX 30-AUG-2000; 2000WO-US023998.
 XX 31-AUG-1999; 99US-0151713P.
 PR 27-SEP-1999; 99US-00406643.
 PR 27-SEP-1999; 99US-0156236P.
 PR 27-SEP-1999; 99US-0156467P.
 PR 08-NOV-1999; 99US-00436430.
 PR 06-DEC-1999; 99US-0169100P.
 PR 29-DEC-1999; 99US-00474432.
 PR 29-DEC-1999; 99US-0173612P.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-00531025.

PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578223.
 PR 09-AUG-2000; 2000US-00636385.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
 PI Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 XX WPI; 2001-244406/25.
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.
 XX Example 1; Page 299; 717pp; English.
 XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a ribozyme used in the examples of the present
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the
 CC specification, but these have different sequences associated with them.

XX SQ Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 5 GGAGTGGATGGCAAGCAGCA 23
 |||||:|||||
 Db 2 GGAGUGAUGGCAUGCAGCA 20

RESULT 32
 AAH96713
 ID AAH96713 standard; RNA; 37 BP.
 XX AAH96713;
 XX 09-OCT-2001 (first entry)
 XX Human Chk1 ribozyme SEQ ID NO: 2138.
 DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
 KW RNA cleavage; cancer; ss.
 XX Homo sapiens.
 XX WO200157206-A2.
 XX 09-AUG-2001.
 XX 02-FEB-2001; 2001WO-US003504.
 XX 03-FEB-2000; 2000US-0179983P.
 XX

PA (RIBO-) RIBOZYME PHARM INC.
 PA (FATT/) FATTAEY A R.
 XX
 PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
 XX
 DR WPI; 2001-496922/54.
 XX
 XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
 PT molecules, which downregulate expression of a checkpoint kinase-1 gene,
 PT useful for treating colorectal, lung, breast or prostate cancers.
 XX
 PS Claim 5; Page 67; 115pp; English.
 XX
 CC The present invention provides nucleic acid molecules capable of
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)
 CC gene. These may be antisense or ribozyme sequences, and are useful in the
 CC treatment of diseases associated with conditions affected by Chk1 levels,
 CC including cancer. The present sequence is an oligonucleotide described in
 CC the exemplification of the invention
 XX
 XX Sequence 37 BP; 9 A; 7 C; 11 G; 0 T; 10 U; 0 Other;
 SQ
 Query Match 65.8%; Score 15.8; DB 4; Length 37;
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 GGAGTGATGGCAAGCACGA 23
 Db ||||:|||||
 5 GGAGUGAUGGCAUGCACUA 23
 RESULT 33
 ABK05427
 ID ABK05427 standard; RNA; 37 BP.
 AC ABK05427;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO G-Cleaver substrate sequence #90.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI
 XX WPI; 2001-607195/69.
 DR
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 XX central nervous system injury.
 XX
 PS Claim 89; Page 93; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;
 Query Match 65.8%; Score 15.8; DB 4; Length 37;
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 GGAGTGATGGCAAGCACGA 23
 Db ||||:|||||
 5 GGAGUGAUGGCAUGCACUA 23
 RESULT 34
 ABK08475
 ID ABK08475 standard; RNA; 37 BP.
 XX
 AC ABK08475;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human CD20 G-Cleaver substrate #34.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;


```
RESULT 36
ABK59178
ID ABK59178 standard; RNA; 37 BP.
XX
XX
AC ABK59178;
XX
XX
02-JUL-2002 (first entry)
XX
XX
Human CLCA1 gene enzymatic nucleic acid #3549.
XX
XX
Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX
XX
antiflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX
XX
chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX
XX
oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX
XX
acetylcysteine.
XX
XX
Homo sapiens.
XX
XX
WO200211674-A2.
XX
XX
14-FEB-2002.
XX
XX
09-AUG-2001; 2001WO-US024970.
XX
XX
09-AUG-2000; 2000US-0224383P.
XX
XX
(RIBO-) RIBOZYME PHARM INC.
XX
XX
(SYNT ) SYNTAX USA LLC.
XX
XX
(THOM/) THOMPSON J.
XX
XX
Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX
XX
Grupe A;
XX
XX
WPI; 2002-217145/27.
XX
XX
Enzymatic polynucleotide that down regulates expression of chloride
XX
XX
channel calcium activated gene, useful for treating Chronic obstructive
XX
XX
pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX
Claim 5; Page 88; 152pp; English.
XX
XX
The invention relates to enzymatic nucleic acid molecules that down
XX
XX
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX
XX
by cleaving RNA derived from the genes. The nucleic acid sequences are
XX
XX
useful as pharmaceutical agents for treating conditions such as chronic
XX
XX
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX
XX
fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX
XX
that are related to or will respond to the levels of CLCA1 in a cell or
XX
XX
tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX
XX
hence, are useful for treatment of a patient having a condition
XX
XX
associated with the level of CLCA1, where the invention further comprises
XX
XX
the use of one or more therapies under conditions suitable for the
XX
XX
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX
XX
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX
XX
nucleic acids of the invention are also used as diagnostic tools to
XX
XX
examine genetic drift and mutations within diseased cells or to detect
XX
XX
the presence of CLCA1 RNA in a cell. This sequence represents an
XX
XX
enzymatic nucleic acid molecule of the invention
XX
XX
Sequence 37 BP; 10 A; 7 C; 12 G; 0 T; 8 U; 0 Other;
XX
XX
Query Match 65.8%; Score 15.8; DB 6; Length 37;
XX
XX
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX
XX
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 5 GGAGTGATGGCAAGCACGA 23
XX
XX
||||:|||||
XX
XX
DB 5 GGAGUGAUGGCAUGCACUA 23
XX
XX
||||:|||||
XX
XX
RESULT 37
ABK59155
ID ABK59155 standard; RNA; 37 BP.
XX
XX
XX
ABK59155;
XX
XX
02-JUL-2002 (first entry)
XX
XX
XX
Human CLCA1 gene enzymatic nucleic acid #3526.
XX
XX
XX
Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX
XX
XX
antiflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX
XX
XX
chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX
XX
XX
oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX
XX
XX
acetylcysteine.
XX
XX
XX
Homo sapiens.
XX
XX
XX
WO200211674-A2.
XX
XX
XX
14-FEB-2002.
XX
XX
XX
09-AUG-2001; 2001WO-US024970.
XX
XX
XX
09-AUG-2000; 2000US-0224383P.
XX
XX
XX
(RIBO-) RIBOZYME PHARM INC.
XX
XX
XX
(SYNT ) SYNTAX USA LLC.
XX
XX
XX
(THOM/) THOMPSON J.
XX
XX
XX
Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX
XX
XX
Grupe A;
XX
XX
XX
WPI; 2002-217145/27.
XX
XX
XX
Enzymatic polynucleotide that down regulates expression of chloride
XX
XX
channel calcium activated gene, useful for treating Chronic obstructive
XX
XX
pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX
XX
Claim 5; Page 87; 152pp; English.
XX
XX
XX
The invention relates to enzymatic nucleic acid molecules that down
XX
XX
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX
XX
by cleaving RNA derived from the genes. The nucleic acid sequences are
XX
XX
useful as pharmaceutical agents for treating conditions such as chronic
XX
XX
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX
XX
fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX
XX
that are related to or will respond to the levels of CLCA1 in a cell or
XX
XX
tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX
XX
hence, are useful for treatment of a patient having a condition
XX
XX
associated with the level of CLCA1, where the invention further comprises
XX
XX
the use of one or more therapies under conditions suitable for the
XX
XX
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX
XX
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX
XX
nucleic acids of the invention are also used as diagnostic tools to
XX
XX
examine genetic drift and mutations within diseased cells or to detect
XX
XX
the presence of CLCA1 RNA in a cell. This sequence represents an
XX
XX
enzymatic nucleic acid molecule of the invention
XX
XX
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XX
XX
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XX
XX
Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX
XX
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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XX
QY 5 GGAGTGATGGCAAGCACGA 23
XX
XX
||||:|||||
XX
XX
DB 5 GGAGUGAUGGCAUGCACUA 23
XX
XX
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XX
XX
RESULT 38
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ID ABK05394 standard; RNA; 37 BP.
XX
XX
XX
ABK05394;
XX
XX
XX
ABK05394;
```

XX 12-MAR-2002 (first entry)
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 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 89; Page 92; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 XX based on the human NOGO sequence
 XX
 SQ Sequence 37 BP; 8 A; 9 C; 12 G; 0 T; 8 U; 0 Other;
 Query Match 65.0%; Score 15.6; DB 4; Length 37;
 Best Local Similarity 72.7%; Pred. No. 1.8e+03;
 Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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 DB 2 AGCGUAUGAUGGCAUGCACUA 23
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 AC ABK05401;
 XX
 DT 12-MAR-2002 (first entry)
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 DE Human NOGO G-Cleaver substrate sequence #64.
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 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
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 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 89; Page 93; 200pp; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence

XX Sequence 37 BP; 11 A; 6 C; 12 G; 0 T; 8 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 4; Length 37;

Best Local Similarity 72.7%; Pred. No. 1.8e+03;

Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGAGTGTATGGCAAGCACA 23

DB 2 AGAGAAGUGAUGGCAUGCACUA 23

RESULT 40

ABK05385

ID ABK05385 standard; RNA; 37 BP.

AC ABK05385;

XX 12-WAR-2002 (first entry)

DT Human NOGO G-Cleaver substrate sequence #48.

DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW musclar; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-0181797P.

PR 26-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

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PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 89; Page 92; 200pp; English.

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CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a substrate sequence for a nucleic acid of the invention

CC based on the human NOGO sequence

XX Sequence 37 BP; 5 A; 7 C; 20 G; 0 T; 5 U; 0 Other;

QY Query Match 65.0%; Score 15.6; DB 4; Length 37;

Best Local Similarity 72.7%; Pred. No. 1.8e+03;

Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGAGTGTATGGCAAGCACA 23

DB 2 AGGGGGGUGAUGGCAUGCACUA 23

Search completed: December 13, 2005, 13:34:14

Job time : 370.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:48:14 ; Search time 1116.5 Seconds
(without alignments)
1221.892 Million cell updates/sec

Title: US-10-713-137-2
Perfect score: 24
Sequence: 1 cagcgagtgatggcaagcagcagc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues 2097806
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_in.*
- 3: gb_env.*
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- 14: gb_htg.*
- 15: gb_pi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6	CS101222 Sequence
2	18.2	75.8	37	6	AX219953 Sequence
3	17.2	71.7	37	6	AX228569 Sequence
4	16.6	69.2	37	6	AX219916 Sequence
5	16.6	69.2	37	6	AX581664 Sequence
6	16.2	67.5	37	6	AX219924 Sequence
7	16.2	67.5	37	6	AX219932 Sequence
8	15.8	65.8	36	6	AR335577 Sequence
9	15.8	65.8	36	6	AR335598 Sequence
10	15.8	65.8	36	6	AR436338 Sequence
11	15.8	65.8	37	6	AX219985 Sequence
12	15.8	65.8	37	6	AX223033 Sequence
13	15.8	65.8	37	6	AX228555 Sequence
14	15.8	65.8	37	6	AX581654 Sequence
15	15.8	65.8	37	6	AX581688 Sequence
16	15.8	65.8	37	6	AX581711 Sequence
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19	15.6	65.0	37	6	AX219959 Sequence
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21	15.2	63.3	36	6	AR335323 Sequence
22	15.2	63.3	36	6	AR336775 Sequence
23	15.2	63.3	36	6	AR336798 Sequence
24	15.2	63.3	36	6	AR436566 Sequence
25	15.2	63.3	36	6	AR436755 Sequence
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27	15.2	63.3	37	6	AX219925 Sequence
28	15.2	63.3	37	6	AX220062 Sequence
29	15.2	63.3	37	6	AX228522 Sequence
30	15.2	63.3	37	6	AX228545 Sequence
31	15.2	63.3	37	6	AX424952 Sequence
32	15.2	63.3	37	6	AX581615 Sequence
33	15	62.5	37	6	AX219897 Sequence
34	15	62.5	37	6	AX219910 Sequence
35	15	62.5	37	6	AX220011 Sequence
36	15	62.5	37	6	AX220100 Sequence
37	15	62.5	37	6	AX220111 Sequence
38	15	62.5	37	6	AX220120 Sequence
39	15	62.5	37	6	AX228609 Sequence
40	15	62.5	37	6	AX228610 Sequence
41	15	62.5	37	6	AX424963 Sequence
42	15	62.5	37	6	AX581739 Sequence
43	15	62.5	37	6	AX581753 Sequence
44	15	62.5	39	6	AR282027 Sequence
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DEFINITION	CS101222					
ACCESSION	CS101222					
VERSION	CS101222.1	GI:67509719				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE	1	Pasha,A.Q. and Ahsan,A.				
AUTHORS		Method of detecting predisposition to high altitude pulmonary edema				
TITLE		Patent: WO 2005047540-A 2 26-MAY-2005;				
JOURNAL		Council of Scientific and Industrial Research (IN)				
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DEFINITION	AX219953			linear
ACCESSION	AX219953			
VERSION	AX219953.1	GI:15547677		
KEYWORDS		synthetic construct		
SOURCE		synthetic construct		
ORGANISM				

other sequences; artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5395 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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DEFINITION Sequence 1941 from Patent WO0157206.
ACCESSION AX228569
VERSION AX228569.1 GI:15557710
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 1941 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)

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DEFINITION Sequence 5358 from Patent WO0159103.
ACCESSION AX219916
VERSION AX219916.1 GI:15547640
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5358 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES
source Location/Qualifiers
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/note="Nucleic Acid"

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Qy 1 CAGCGGAGTGTGGCAAGCAGCA 23
||| ||||| ||||| ||||| |||||
Db 1 CAGGGCGGTGATGCATGCACTA 23

RESULT 5
AX581664
LOCUS AX581664 37 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 3502 from Patent WO0211674.
ACCESSION AX581664
VERSION AX581664.1 GI:27653474
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)
JOURNAL Patent: WO 0211674-A 3502 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)

FEATURES
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1. .37
/organism="synthetic construct"
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ORIGIN
Query Match 69.2%; Score 16.6; DB 6; Length 37;
Best Local Similarity 82.6%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCAGCA 23
||| ||||| ||||| ||||| |||||
Db 1 CAGGCTAGTGTGATGCATGCACTA 23

RESULT 6
AX219924
LOCUS AX219924 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5366 from Patent WO0159103.
ACCESSION AX219924
VERSION AX219924.1 GI:15547648
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5366 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match          67.5%; Score 16.2; DB 6; Length 37;
Best Local Similarity 85.7%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  3 GCGGAGTGATGGCAAGCAGCA 23
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Db   3 GCGGAGTGATGGCATGCACTA 23
    |||||

RESULT 7
AX425032
LOCUS          37 bp RNA linear PAT 18-JUN-2002
DEFINITION    Sequence 3368 from Patent WO0188124.
ACCESSION     AX425032
VERSION       AX425032.1 GI:21528414
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Jarvis,T., von Carlowitz,I., McSwiggen,J.A., McLaughlin,F.G. and
               Randi,A.M.
TITLE         Method and reagent for the inhibition of erg
JOURNAL       Patent: WO 0188124-A 3368 22-NOV-2001;
               RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES      Location/Qualifiers
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               /db_xref="taxon:32630"
               /note="Enzymatic Nucleic Acid"

ORIGIN
Query Match          67.5%; Score 16.2; DB 6; Length 37;
Best Local Similarity 85.7%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  3 GCGGAGTGATGGCAAGCAGCA 23
    |||||
Db   3 GCGTAGTGATGGCATGCACTA 23
    |||||

RESULT 8
AX335577
LOCUS          36 bp RNA linear PAT 17-AUG-2003
DEFINITION    Sequence 12979 from patent US 6566127.
ACCESSION     AR335577
VERSION       AR335577.1 GI:33721385
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 36)
AUTHORS       Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE         Method and reagent for the treatment of diseases or conditions
               related to levels of vascular endothelial growth factor receptor
JOURNAL       Patent: US 6566127-A 12979 20-MAY-2003;
               Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES      Location/Qualifiers
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               1..36
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               /mol_type="unassigned RNA"

ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GGAGTGATGGCAAGCAGCA 23
    |||||
Db   2 GGAGTGATGGCATGCACTA 20
    |||||

RESULT 9
AX335598
LOCUS          36 bp RNA linear PAT 17-AUG-2003
DEFINITION    Sequence 13000 from patent US 6566127.
ACCESSION     AR335598
VERSION       AR335598.1 GI:33721406
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 36)
AUTHORS       Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE         Method and reagent for the treatment of diseases or conditions
               related to levels of vascular endothelial growth factor receptor
JOURNAL       Patent: US 6566127-A 13000 20-MAY-2003;
               Ribozyme Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES      Location/Qualifiers
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ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GGAGTGATGGCAAGCAGCA 23
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Db   2 GGAGTGATGGCATGCACTA 20
    |||||

RESULT 10
AX436338
LOCUS          36 bp RNA linear PAT 18-DEC-2003
DEFINITION    Sequence 597 from patent US 6656731.
ACCESSION     AR436338
VERSION       AR436338.1 GI:40199422
KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 36)
AUTHORS       Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE         Nucleic acid catalysts with endonuclease activity
JOURNAL       Patent: US 6656731-A 597 02-DEC-2003;
               Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
               Sirna Therapeutics; Munich;
               DEX;
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ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GGAGTGATGGCAAGCAGCA 23
    |||||
Db   2 GGAGTGATGGCATGCACTA 20
    |||||

RESULT 11
AX219985
LOCUS          37 bp RNA linear PAT 07-SEP-2001
DEFINITION    Sequence 5427 from Patent WO0159103.
ACCESSION     AX219985
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FEATURES
source
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
Location/Qualifiers
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
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Db 5 GGAGTGATGGCATGCACTA 23

RESULT 16
AX581711
LOCUS AX581711 37 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 3549 from Patent WO0211674.
ACCESSION AX581711
VERSION AX581711.1 GI:27653521
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (Cicca-1)
JOURNAL Patent: WO 0211674-A 3549 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
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Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
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Db 5 GGAGTGATGGCATGCACTA 23

RESULT 17
AX219943
LOCUS AX219943 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5385 from Patent WO0159103.
ACCESSION AX219943
VERSION AX219943.1 GI:15547667
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5385 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
Location/Qualifiers
1. .37

ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 37;
Best Local Similarity 81.8%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGTGATGGCAAGCACGA 23
|||||
Db 2 AGCGGGTGATGGCATGCACTA 23

RESULT 18
AX219952
LOCUS AX219952 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5394 from Patent WO0159103.
ACCESSION AX219952
VERSION AX219952.1 GI:15547676
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5394 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
Location/Qualifiers
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 65.0%; Score 15.6; DB 6; Length 37;
Best Local Similarity 81.8%; Pred. No. 3.2e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGTGATGGCAAGCACGA 23
|||||
Db 2 AGCGTATTGATGGCATGCACTA 23

RESULT 19
AX219959
LOCUS AX219959 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5401 from Patent WO0159103.
ACCESSION AX219959
VERSION AX219959.1 GI:15547683
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5401 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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/mol_type="unassigned RNA"
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/note="Nucleic Acid"

ORIGIN

TITLE Nucleic acid catalysts with endonuclease activity
JOURNAL Patent: US 6656731-A 825 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
DEX;

FEATURES source Location/Qualifiers
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/mol_type="unassigned RNA"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 36;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CGGAGTGATGGCAAGCACGA 23
Db 1 CGTAGTGATGGCATGCACTA 20

RESULT 25
LOCUS AR436755 36 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 1014 from patent US 6656731.
ACCESSION AR436755
VERSION AR436755.1 GI:40199839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE Nucleic acid catalysts with endonuclease activity
JOURNAL Patent: US 6656731-A 1014 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
DEX;

FEATURES source Location/Qualifiers
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ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 36;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CGGAGTGATGGCAAGCACGA 23
Db 1 CGGGGTGATGGCATGCACTA 20

RESULT 26
LOCUS AX219922 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5364 from Patent WO0159103.
ACCESSION AX219922
VERSION AX219922.1 GI:15547646
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 5364 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"

/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CGGAGTGATGGCAAGCACGA 23
Db 4 CGGGGTGATGGCATGCACTA 23

RESULT 27
LOCUS AX219925 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5367 from Patent WO0159103.
ACCESSION AX219925
VERSION AX219925.1 GI:15547649
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 5367 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES source Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 CGGAGTGATGGCAAGCACGA 23
Db 4 CGGGGTGATGGCATGCACTA 23

RESULT 28
LOCUS AX220062 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5504 from Patent WO0159103.
ACCESSION AX220062
VERSION AX220062.1 GI:15547786
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 5504 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES source Location/Qualifiers
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/note="Nucleic Acid"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;

Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
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Db 4 CCGGGTGATGGCATGCACTA 23

RESULT 29
AX228522
LOCUS AX228522 37 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 1894 from Patent WO0157206.
ACCESSION AX228522
VERSION AX228522.1 GI:15557663
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fattaey, A.R., Jarvis, T., Mcswiggen, J., Boohar, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 1894 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
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1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
|||||
Db 4 CCGAGTGATGGCATGCACTA 23

RESULT 30
AX228545
LOCUS AX228545 37 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 1917 from Patent WO0157206.
ACCESSION AX228545
VERSION AX228545.1 GI:15557686
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fattaey, A.R., Jarvis, T., Mcswiggen, J., Boohar, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme
JOURNAL Patent: WO 0157206-A 1917 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
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ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
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Db 4 CTGAGTGATGGCATGCACTA 23

RESULT 31

AX424952
LOCUS AX424952 37 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 3288 from Patent WO0188124.
ACCESSION AX424952
VERSION AX424952.1 GI:21528334
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, P.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 3288 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
|||||
Db 4 CCGGGTGATGGCATGCACTA 23

RESULT 32
AX581615
LOCUS AX581615 37 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 3453 from Patent WO0211674.
ACCESSION AX581615
VERSION AX581615.1 GI:27653425
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3453 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
FEATURES
source
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
|||||
Db 4 CCGATTGATGGCATGCACTA 23

RESULT 33
AX219897
LOCUS AX219897 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5339 from Patent WO0159103.
ACCESSION AX219897
VERSION AX219897.1 GI:15547621

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Query Match 62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACGGGAGTGATGGCAAGCACGA 23
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DB 1 CACGGAAGTGATGGCATGCACCTA 23

RESULT 36
AX220100 37 bp RNA linear PAT 07-SEP-2001

LOCUS
DEFINITION Sequence 5542 from Patent WO0159103.
ACCESSION AX220100
VERSION AX220100.1 GI:15547824
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
1 other sequences; artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5542 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Query Match 62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACGGGAGTGATGGCAAGCACGA 23
||| ||||| ||||| |||||
DB 1 CAGAGAATTGATGGCATGCACCTA 23

RESULT 37
AX220111 37 bp RNA linear PAT 07-SEP-2001

LOCUS
DEFINITION Sequence 5553 from Patent WO0159103.
ACCESSION AX220111
VERSION AX220111.1 GI:15547835
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
1 other sequences; artificial sequences.

REFERENCE
1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 5553 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

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McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Nucleic Acid"
ORIGIN
Query Match      62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
    ||| ||||| ||||| ||||| |||||
Db 1 CAGCTTTGTGATGGCATGCACTA 23
    ||| ||||| ||||| ||||| |||||
RESULT 38
AX220120          AX220120          37 bp      RNA          linear      PAT 07-SEP-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Blatt L., McSwiggen, J. and Chowrira, B.M.
TITLE
  Method and reagent for the modulation and diagnosis of cd20 and
  nogo gene expression
JOURNAL
  Patent: WO 0159103-A 5562 16-AUG-2001;
  RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
  McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Nucleic Acid"
ORIGIN
Query Match      62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
    ||| ||||| ||||| ||||| |||||
Db 1 CAACAGTGTGATGGCATGCACTA 23
    ||| ||||| ||||| ||||| |||||
RESULT 39
AX228609          AX228609          37 bp      RNA          linear      PAT 10-SEP-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE
  Method and reagent for the inhibition of checkpoint kinase-1 (chk
  1) enzyme
JOURNAL
  Patent: WO 0157206-A 1981 09-AUG-2001;
  RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"

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```

ORIGIN
Query Match      62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
    ||| ||||| ||||| ||||| |||||
Db 1 CATAGCAGTGATGGCATGCACTA 23
    ||| ||||| ||||| ||||| |||||
RESULT 40
AX228610          AX228610          37 bp      RNA          linear      PAT 10-SEP-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct
    other sequences; artificial sequences.
REFERENCE
  1
AUTHORS
  Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE
  Method and reagent for the inhibition of checkpoint kinase-1 (chk
  1) enzyme
JOURNAL
  Patent: WO 0157206-A 1982 09-AUG-2001;
  RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
ORIGIN
Query Match      62.5%; Score 15; DB 6; Length 37;
Best Local Similarity 78.3%; Pred. No. 6.1e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
    ||| ||||| ||||| ||||| |||||
Db 1 CAACATAGTGATGGCATGCACTA 23
    ||| ||||| ||||| ||||| |||||
Search completed: December 13, 2005, 14:11:38
Job time : 1118.5 secs

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 253506
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-253506
```

```
Query Match 61.7%; Score 14.8; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 TGCACAGCTGGGGAACA 20
Db 2 UGCACAGCUGGGGACAA 19
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```
RESULT 3
US-11-101-244-126494
; Sequence 126494, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 126494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-126494
```

```
Query Match 60.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GCACAGCTGGGGAACA 19
Db 3 GCACAGCUGGGGGAAGA 18
```

```
RESULT 4
US-11-083-784-126494
; Sequence 126494, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 126494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-126494
```

```
Query Match 60.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GCACAGCTGGGGAACA 19
Db 3 GCACAGCUGGGGGAAGA 18
```

```
RESULT 5
US-10-508-932-36/C
; Sequence 36, Application US/10508932
; Publication No. US20050260586A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Weaver, David A.
; APPLICANT: Warner, Kristy A.
; APPLICANT: Graves, Timothy G.
; APPLICANT: Demuth, Jeffrey P.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: Method and Compositions for the Diagnosis and Treatment of Non-S.
; TITLE OF INVENTION: Lung Cancer Using Gene Expression Profiles
; FILE REFERENCE: 9050
; CURRENT APPLICATION NUMBER: US/10/508,932
; CURRENT FILING DATE: 2004-09-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-508-932-36
```

```
Query Match 60.0%; Score 14.4; DB 6; Length 42;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 GATCACAGCTGGGGAACAAGACG 24
Db 37 GATGAGAGAGGGGACCAAGAG 14
```

```
RESULT 6
US-11-101-244-314817
; Sequence 314817, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 314817
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-314817
```

```
Query Match      59.2%; Score 14.2; DB 9; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.6e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGAACAAGA 22
|||||: |||||
Db 1 GCACAGCTCAGGAACUAGA 19
```

```
RESULT 7
US-11-083-784-314817
; Sequence 314817, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 314817
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-314817
```

```
Query Match      59.2%; Score 14.2; DB 9; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.6e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGAACAAGA 22
|||||: |||||
Db 1 GCACAGCTCAGGAACUAGA 19
```

```
RESULT 8
US-11-101-244-253501
; Sequence 253501, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 253501
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-253501
```

```
Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGAACAA 20
|||||: |||||
Db 1 GCACAGCTGAGGGACAA 17
```

```
RESULT 9
US-11-101-244-452572
; Sequence 452572, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-452572
```

```
Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGAACAA 20
|||||: |||||
Db 3 GCACAGCTGGGGAACAA 19
```

```
RESULT 10
US-11-101-244-452581
; Sequence 452581, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 432581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-452581

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 GCACAGCTGGGGAACAA 20
      |||||:|||||
Db      1 GCACACGUGGUAUCAA 17

```

```

RESULT 11
US-11-101-244-639666
; Sequence 639666, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 639666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-639666

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 TGCACAGCTGGGGAACA 19
      :|||||:|:|||||
Db      2 UGCACACGUGGAGAACAA 18

```

```

RESULT 12
US-11-101-244-940716
; Sequence 940716, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-940716

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 ACAGCTGGGGAACAAGA 22
      |||||:|||||
Db      2 AAAGCUGAGGAACAAGA 18

```

```

RESULT 13
US-11-101-244-940758
; Sequence 940758, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-940758

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 ACAGCTGGGGAACAAGA 22
      |||||:|||||
Db      3 AAAGCUGAGGAACAAGA 19

```

```

RESULT 14
US-11-101-244-987947
; Sequence 987947, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 987947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-987947

Query Match 57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAACAGA 22
| | | | | | | | | | | | | | | | | | | | |
Db 3 ACAGCUGGUAUAAGA 19

RESULT 15
US-11-083-784-253501
; Sequence 253501, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 253501
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-253501

Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAA 20
| | | | | | | | | | | | | | | | | | | | |
Db 1 GCACAGCUGAGGACAA 17

RESULT 16
US-11-083-784-452572
; Sequence 452572, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-452572

Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAA 20
| | | | | | | | | | | | | | | | | | | | |
Db 3 GCACAGCUGGUAUCA 19

RESULT 17
US-11-083-784-452581
; Sequence 452581, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-452581

Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAA 20
| | | | | | | | | | | | | | | | | | | | |
Db 1 GCACAGCUGGUAUCA 17

RESULT 18
US-11-083-784-639666
; Sequence 639666, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 639666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-639666
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 TCACACGCTGGGGAACA 19
   :|||||:|||||
Db 2 UGCACACCTUGGAGACA 18
```

RESULT 19

```
US-11-083-784-940716
; Sequence 940716, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-940716
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 2 AAAGCUGAGGACACAGA 18
```

RESULT 20

```
US-11-083-784-940758
; Sequence 940758, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-940758
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 3 AAAGCUGAGGACACAGA 19
```

RESULT 21

```
US-11-083-784-987947
; Sequence 987947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 987947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-987947
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 3 ACAGCUGGGAUAAAGA 19
```

RESULT 22

```
US-10-770-726-10883/c
```

```
; Sequence 10883, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10770726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10883
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-10883

Query Match      56.7%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 TGCACAGCTGGGGAACAAGA 22
Db      20 TCCACAGCTGTGGAATAATA 1

RESULT 23
US-11-101-244-387702
; Sequence 387702, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387702
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387702

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CACAGCTGGGGAACA 19
Db      4 CACAGCUGGUGAACA 18

RESULT 24
US-11-101-244-387807
; Sequence 387807, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387807

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CACAGCTGGGGAACA 19
Db      4 CACAGCUGGUGAACA 18

RESULT 25
US-11-101-244-387902
; Sequence 387902, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387902
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387902

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CACAGCTGGGGAACA 19
Db      4 CACAGCUGGUGAACA 18

RESULT 26
US-11-101-244-503486
; Sequence 503486, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 503486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-503486
```

```
Query Match 55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 TGACAGCTGGGCAA 17
    :|||||:|||||
Db 2 UGCACGUGGAGAA 16
```

```
RESULT 27
US-11-083-784-387702
; Sequence 387702, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387702
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387702
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    :|||||:|||||
Db 4 CACAGCUGGGAACA 18
```

```
RESULT 28
US-11-083-784-387807
; Sequence 387807, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387807
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    :|||||:|||||
Db 4 CACAGCUGGGAACA 18
```

```
RESULT 29
US-11-083-784-387902
; Sequence 387902, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387902
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387902
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    :|||||:|||||
Db 4 CACAGCUGGGAACA 18
```

```
RESULT 30
US-11-083-784-503486
; Sequence 503486, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 503486
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-503486

Query Match 55.8%; Score 13.4; DB 9; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAA 17
 :|||||: |||
 Db 2 UGCACAGCUGGAGAA 16

RESULT 31
 US-11-101-244-92175/c
 ; Sequence 92175, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmakon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 92175
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-92175

Query Match 55.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAAACAAGAC 23
 :|||||: |||||
 Db 19 AAATCTGGGAAACAAGAC 2

RESULT 32
 US-11-101-244-624295
 ; Sequence 624295, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:

; APPLICANT: Dharmakon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 624295
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-624295

Query Match 55.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 72.2%; Pred. No. 2.2e+03;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAAACAA 20
 :|||||: ||| |||
 Db 2 UGCACACUGGAGAGAA 19

RESULT 33
 US-11-101-244-1302115
 ; Sequence 1302115, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmakon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1302115
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1302115

Query Match 55.0%; Score 13.2; DB 8; Length 19;
 Best Local Similarity 72.2%; Pred. No. 2.2e+03;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAAACAA 20
 :|||: |||: |||
 Db 2 UGCACAGCUGGGAACCAA 19

RESULT 34
 US-11-101-244-1313799
 ; Sequence 1313799, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:

; APPLICANT: Dharmakon, Inc.


```

: APPLICANT: Khvorova, Anastasia
: APPLICANT: Reynolds, Angela
: APPLICANT: Leake, Devin
: APPLICANT: Marshall, William
: APPLICANT: Scaringe, Stephen
: TITLE OF INVENTION: Functional and Hyperfunctional siRNA
: FILE REFERENCE: 134990S
: CURRENT APPLICATION NUMBER: US/11/101,244
: CURRENT FILING DATE: 2005-04-07
: PRIOR APPLICATION NUMBER: 60/502,050
: PRIOR FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/426,137
: PRIOR FILING DATE: 2002-11-14
: NUMBER OF SEQ ID NOS: 1591911
: SOFTWARE: Proprietary
: SEQ ID NO 1313799
: LENGTH: 19
: TYPE: RNA
: ORGANISM: Homo sapiens
US-11-101-244-1313799

```

Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 2; Mismatches 3; Indels

Qy 3 TGCACAGCTGGGAACAA 20
:|:|:|:|:|:|:|
Db 2 UGCUCUGCUGAGGAACAA 19

```

RESULT 35
US-11-101-244-1313893
; Sequence 1313893, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Khorova, Devin
; APPLICANT: Leake, William
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: PROPRIETARY
; SEQ ID NO 1313893
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1313893

```

Query Match	55.0%	Score 13.2;	DB 8;
Best Local Similarity	72.2%	Pred. No. 2.2e+03;	
Matches 13; Conservative	2;	Mismatches 3	Indels

Qy 3 TGCA CAGCTGGGGAACAA 20
: : : : : : : : : :
pb 2 UGCUCUGCUGAGGGAACAA 19

RESULT 36
US-11-101-244-1345869
; Sequence 1345869, Application US/11010244
; Publication No. US20050346794A1
; GENERAL INFORMATION:
; APPLICANT: Khmarcon, Inc.
; APPLICANT: Khmarcon, Anastasia

```

, APPLICANT: Reynolds, Angela
, APPLICANT: Leake, Devin
, APPLICANT: Marshall, William
, APPLICANT: Scaringe, Stephen
, TITLE OF INVENTION: Functional and Hyperfunctional siRNA
, FILE REFERENCE: 1349SUS
, CURRENT APPLICATION NUMBER: US/11/101,244
, CURRENT FILING DATE: 2005-04-07
, PRIOR APPLICATION NUMBER: 60/502,050
, PRIOR FILING DATE: 2003-09-10
, PRIOR APPLICATION NUMBER: 60/426,137
, PRIOR FILING DATE: 2002-11-14
, NUMBER OF SEQ ID NOS: 159111
, SOFTWARE: Proprietary
, SEQ ID NO 1345869
, LENGTH: 19
, TYPE: RNA
, ORGANISM: Homo sapiens
US-11-101-244-1345869

```

Query Match	55.0%;	Score 13.2;	DB 8;	Length 19;
Best Local Similarity	77.8%;	Pred. No. 2.2e+03;		
Matches 14;	Conservative	1;	Mismatches 3;	Indels 0;
				Gaps 0;

QY 5 CACAGCTGGGGAACAAGA 22
| | | | | : | | | | |
Db 2 CACAGCUGGUGAGGAAGA 19

```

RESULT 37
US-11-101-244-1360531
; Sequence 1360531, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Kharmacon, Inc.
; APPLICANT: Dhorotova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Keayles, Devin
; APPLICANT: Leake, William
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1360531
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1360531

```

Query Match	55.0%	Score 13.2;	DB 8;	Length 19;
Best Local Similarity	77.8%	Pred. No. 2.2e+03;		
Matches 14;	Conservative	1;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 5 CACAGCTGGGGAACAAGA 22
|||||:|||||
Db 2 CACAGCTUAGGGAGAAAAGA 19

RESULT 38
US-11-101-244-1526049
; Sequence 1526049, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1526049
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1526049
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.2e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 ACAGCTGGGGAACAAGAC 23
Db 2 AAAGUUGGAGAACAAAGAC 19
|||:|||||
|||:|||||
```

RESULT 39

```
US-11-101-244-1529226
; Sequence 1529226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1529226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1529226
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 TGCACAGCTGGGGAACAA 20
Db 2 UGAACAGCUGUGGAUAA 19
:|||||:|||||
```

RESULT 40

```
US-11-083-784-92175/c
; Sequence 92175, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 92175
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-92175
```

```
Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 ACAGCTGGGGAACAAGAC 23
Db 19 AAATCTGGGGAACAAGAC 2
|||||:|||||
|||||:|||||
```

Search completed: December 13, 2005, 16:24:35
Job time : 215.5 secs

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